

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2006, 01:14:37 ; Search time 3379 Seconds
(without alignments)
8667.629 Million cell updates/sec

Title: US-10-719-996A-2

Perfect score: 458
Sequence: 1 atgactcgagactgcgttcgag.....cgtcaggtctcgagactcgc 458

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 segs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seg length: 0

Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBdb1:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	458	100.0	458	2	AX958629	AX958629 Sequence
2	458	100.0	458	2	AX685342	AX685342 Sequence
3	458	100.0	472	2	AX963308	AX963308 Sequence
4	317	69.2	447	2	AX958630	AX958630 Sequence
5	317	69.2	447	2	AX963309	AX963309 Sequence
6	317	69.2	447	2	AX685343	AX685343 Sequence
7	291.6	63.7	429	2	AX958628	AX958628 Sequence
8	291.6	63.7	429	2	AX685341	AX685341 Sequence
9	291.6	63.7	1468	15	ATUDROS	M65201 A. tumefaci
10	271.4	59.3	10212	15	AE008022	AE008022 Agrobacte
11	271.4	59.3	10229	15	AE009056	AE009056 Agrobacte
12	270	59.0	783	15	ARROS	X82941 A. radiobact
13	212.2	46.3	856	15	AY683454	AY683454 Rhizobium
14	212.2	46.0	1174	15	AY683453	AY683453 Rhizobium
15	210.6	43.2	432	15	RME237844	AJ237844 Rhizobium
16	209	45.6	3602	15	L37353	L37353 Sinorhizobi
17	209	45.6	286550	15	SME591785	AL591785 Sinorhizo
18	202.6	44.2	1935	15	REU61146	U61146 Rhizobium e

19	202.6	44.2	110000	15	CP000133_12	Continuation (13 o
20	202.6	44.2	110000	15	CP000133_13	Continuation (14 o
21	199.4	43.5	110000	15	U00090_0	U00090 Rhizobium s
22	199.4	43.5	320040	2	A79350	A79350 Sequence 1
23	199.4	43.5	320040	2	A93002	A93002 Sequence 1
24	196.2	42.8	169168	11	BX546502	BX546502 Zebrafish
25	138.4	30.2	110000	15	AE014291_05	Continuation (6 of
26	136.8	29.9	10305	15	AE009574	AE009574 Brucella
27	136.8	29.9	110000	15	AE017223_05	Continuation (6 of
28	136.8	29.9	110000	15	AE040264_05	Continuation (6 of
29	127.8	27.9	110000	15	BX897699_05	Continuation (6 of
30	121.8	26.3	346879	15	BX572598	BX572598 Rhodospes
31	120.6	26.3	110000	15	BA000012_63	Continuation (64 o
32	118	25.8	110000	15	BA000012_49	Continuation (50 o
33	116.4	25.4	152050	15	ML0672113	AL672113 Mesorhizo
34	113.4	24.8	10886	15	AE005772	AE005772 Caulobact
35	112.4	24.5	110000	15	CP000115_24	Continuation (25 o
36	112.4	24.5	110000	15	BA000012_50	Continuation (51 o
37	111	24.2	110000	15	BX897700_04	Continuation (5 of
38	106	23.1	110000	15	AE006692_14	Continuation (15 o
39	105	22.9	110000	15	CP000248_10	Continuation (11 o
40	103.6	22.6	110000	15	BA000040_33	Continuation (34 o
41	101.2	22.1	52825	15	CP000230_43	Continuation (44 o
42	100	21.8	110000	15	CP000157_17	Continuation (18 o
43	99.6	21.7	10664	15	AE007231	AE007231 Sinorhizo
44	99.4	21.7	110000	15	BA000013_0	BA000013 Mesorhizo
45	98.6	21.5	110000	15	CP000250_40	Continuation (41 o

ALIGNMENTS

RESULT 1	AX958629	458 bp	DNA	linear	PAT 14-JAN-2004
LOCUS	AX958629	Sequence 2 from Patent WO03100063.			
DEFINITION	AX958629				
ACCESSION	AX958629				
VERSION	AX958629.1	GI:40879469			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE	1				
AUTHORS	Hannoufa, A., Hegedus, D. and Bate, N.				
TITLE	A repressor-mediated regulation system for control of gene expression in plants				
JOURNAL	Patent: WO 03100063-A 2 04-DEC-2003;				
	Her Majesty The Queen in Right of Canada, as Represented; by The Minister of Agriculture and Agri-Food (CA)				
FEATURES	Location/Qualifiers				
source	1..458				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="synthetic ROS optimized for plant codon usage and encoding fusion of ROS and nuclear localization signal"				
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Query Match	100.0%; Score 458; DB 2; Length 458;				
Best Local Similarity	100.0%; Pred. No. 1.2e-129; Mismatches 0; Indels 0; Gaps 0;				
Matches	458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 ATGACTGAGACTGCTTACGCTTAACGCTCAAGATCTTCTGTTGAGCTTACTGCTGATATC 60				
DB	1 ATGACTGAGACTGCTTACGCTTAACGCTCAAGATCTTCTGTTGAGCTTACTGCTGATATC 60				
QY	61 GTTGCGCTTACGCTTCTTAACCAAGTGTTCCTGTTACGAGCTTCTGAGCTATCTCT 120				
DB	61 GTTGCGCTTACGCTTCTTAACCAAGTGTTCCTGTTACGAGCTTCTGAGCTATCTCT 120				
QY	121 GATGTCATACCTGACCTTCTGGAACATGCTCTGCTTCTGCTGCTTAAAGTTGAG 180				
DB	121 GATGTCATACCTGACCTTCTGGAACATGCTCTGCTTCTGCTGCTTAAAGTTGAG 180				

QY 181 AAGCAGAGCCTGCTGTTCTGTTCTGTAAGTCTGTTCAGGATGATCATATCGTTGTTG 240
DB 181 AAGCAGAGCCTGCTGTTCTGTTCTGTAAGTCTGTTCAGGATGATCATATCGTTGTTG 240
QY 241 GAGTGTGAGTGTCTTCTCAAGTCTCTCAAGCGTCACTTACTACTACTCTATGACT 300
DB 241 GAGTGTGAGTGTCTTCTCAAGTCTCTCAAGCGTCACTTACTACTACTCTATGACT 300
QY 301 CCAGAGAGATATAGAGAGAGTGGATCTTCCTGTTAATTAACCTATAGTTCCTCCGCT 360
DB 301 CCAGAGAGATATAGAGAGAGTGGATCTTCCTGTTAATTAACCTATAGTTCCTCCGCT 360
QY 361 TAGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCTCGTCAAGCTCTGTAAGCT 420
DB 361 TAGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCTCGTCAAGCTCTGTAAGCT 420
QY 421 AACCGTCCAAAAAAGAACGCTAAGCTCTGAGAGCTCCG 458
DB 421 AACCGTCCAAAAAAGAACGCTAAGCTCTGAGAGCTCCG 458

RESULT 2
AX685342 458 bp DNA linear PAT 29-MAR-2003
LOCUS
DEFINITION Sequence 2 from Patent WO02095021.
ACCESSION AX685342
VERSION AX685342.1 GI:29371665
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1
Hannoufa, A., Hegedus, D. and Bate, N.
A repressor-mediated regulation system for control of gene
expression in plants
Patent: WO 02095021-A 2 28-NOV-2002;
The Minister of Agriculture and Agri-Food Canada (CA)
Location/Qualifiers
1. 458
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic ROS optimized for plant codon usage and
encoding fusion of ROS and nuclear localization signal"

ORIGIN
Query Match 100.0%; Score 458; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.2e-129;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACCGTAAGCTCAGAGATCTTCTGTTGAGCTTACTGATATC 60
DB 1 ATGACTGAGACTGCTTACCGTAAGCTCAGAGATCTTCTGTTGAGCTTACTGATATC 60
QY 61 GTTGCTGCTTACGTTCTTAACCAAGTGTCTGTTACTGAGCTTCTGGAATTATCTCT 120
DB 61 GTTGCTGCTTACGTTCTTAACCAAGTGTCTGTTACTGAGCTTCTGGAATTATCTCT 120
QY 121 GATGTTCACTGCACTTCTGGAACATCTGCTCTGTTGCTGTTAAGCTTGGAG 180
DB 121 GATGTTCACTGCACTTCTGGAACATCTGCTCTGTTGCTGTTAAGCTTGGAG 180
QY 181 AAGGAGAGGCTGCTGTTCTGTAAGTCTGTGAGATGATGATCATATGTTGTTG 240
DB 181 AAGGAGAGGCTGCTGTTCTGTAAGTCTGTGAGATGATGATCATATGTTGTTG 240
QY 241 GAGTGTGAGTGTCTTCAAGTCTCTCAAGCGTCACTTACTACTACTCTATGACT 300
DB 241 GAGTGTGAGTGTCTTCAAGTCTCTCAAGCGTCACTTACTACTACTCTATGACT 300
QY 301 CCAGAGAGATATAGAGAGAGTGGATCTTCCTGTTAATTAACCTATAGTTCCTCCGCT 360
DB 301 CCAGAGAGATATAGAGAGAGTGGATCTTCCTGTTAATTAACCTATAGTTCCTCCGCT 360

DB 301 CCAGAGAGATATAGAGAGAGTGGATCTTCCTGTTAATTAACCTATAGTTCCTCCGCT 360
QY 361 TAGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCTCGTCAAGCTCTGTAAGCT 420
DB 361 TAGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCTCGTCAAGCTCTGTAAGCT 420
QY 421 AACCGTCCAAAAAAGAACGCTAAGCTCTGAGAGCTCCG 458
DB 421 AACCGTCCAAAAAAGAACGCTAAGCTCTGAGAGCTCCG 458

RESULT 3
AX963308 472 bp DNA linear PAT 14-JAN-2004
LOCUS
DEFINITION Sequence 2 from Patent WO03104462.
ACCESSION AX963308
VERSION AX963308.1 GI:40882061
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1
Hannoufa, A., Lydiatte, D.J. and Gao, M.J.
Regulation of gene expression using chromatin remodeling factors
Patent: WO 03104462-A 2 18-DEC-2003;
Her Majesty The Queen in Right of Canada, as represented; by The
Minister of Agriculture and Agri-Food Canada (CA)
Location/Qualifiers
1. 472
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic ROS"

ORIGIN

Query Match 100.0%; Score 458; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.2e-129;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACCGTAAGCTCAGAGATCTTCTGTTGAGCTTACTGATATC 60
DB 1 ATGACTGAGACTGCTTACCGTAAGCTCAGAGATCTTCTGTTGAGCTTACTGATATC 74
QY 61 GTTGCTGCTTACGTTCTTAACCAAGTGTCTGTTACTGAGCTTCTGGAATTATCTCT 120
DB 61 GTTGCTGCTTACGTTCTTAACCAAGTGTCTGTTACTGAGCTTCTGGAATTATCTCT 134
QY 121 GATGTTCACTGCACTTCTGGAACATCTGCTCTGTTGCTGTTAAGCTTGGAG 180
DB 121 GATGTTCACTGCACTTCTGGAACATCTGCTCTGTTGCTGTTAAGCTTGGAG 194
QY 181 AAGGAGAGGCTGCTGTTCTGTAAGTCTGTGAGATGATGATCATATGTTGTTG 240
DB 181 AAGGAGAGGCTGCTGTTCTGTAAGTCTGTGAGATGATGATCATATGTTGTTG 254
QY 241 GAGTGTGAGTGTCTTCAAGTCTCTCAAGCGTCACTTACTACTACTCTATGACT 300
DB 241 GAGTGTGAGTGTCTTCAAGTCTCTCAAGCGTCACTTACTACTACTCTATGACT 314
QY 301 CCAGAGAGATATAGAGAGAGTGGATCTTCCTGTTAATTAACCTATAGTTCCTCCGCT 360
DB 301 CCAGAGAGATATAGAGAGAGTGGATCTTCCTGTTAATTAACCTATAGTTCCTCCGCT 374
QY 361 TAGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCTCGTCAAGCTCTGTAAGCT 420
DB 361 TAGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCTCGTCAAGCTCTGTAAGCT 434
QY 421 AACCGTCCAAAAAAGAACGCTAAGCTCTGAGAGCTCCG 458
DB 421 AACCGTCCAAAAAAGAACGCTAAGCTCTGAGAGCTCCG 472

RESULT 4

AX958630	LOCUS	AX958630	447 bp	DNA	linear	PAT 14-JAN-2004
AX958630	DEFINITION	Sequence 3 from Patent WO03100063.				
AX958630	ACCESSION	AX958630.1				
AX958630	VERSION	GI:40879470				
AX958630	KEYWORDS	.				
AX958630	SOURCE	synthetic construct				
AX958630	ORGANISM	synthetic construct				
AX958630	REFERENCE	other sequences; artificial sequences.				
AX958630	AUTHORS	1				
AX958630	TITLE	Hannoufa, A., Hegedus, D. and Bate, N.				
AX958630	JOURNAL	A repressor-mediated regulation system for control of gene expression in plants				
AX958630	FEATURES	Patent: WO 03100063-A 3 04-DEC-2003;				
AX958630	source	Her Majesty The Queen in Right of Canada, as Represented, by The Minister of Agriculture and Agri-Food (CA)				
AX958630	ORIGIN	Location/Qualifiers				
AX958630	Query Match	1..447				
AX958630	Match Local Similarity	/organism="synthetic construct"				
AX958630	Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;	/mol_type="unassigned DNA"				
AX958630		/db_xref="caxon:32630"				
AX958630		/note="ROS consensus sequence"				
AX958630		69.2%; Score 317; DB 2; Length 447;				
AX958630		58.3%; Pred. No. 3.3e-86;				
AX958630		Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;				
AX958630		1 ATGACTGAGCTGCTTACCGCTGAGATCTCTTGTGAGCTTACTGCTGATATC 60				
AX958630		1 ATGACNGRACNGCTTATGNNAAVNCNARGAATYNTNGTNGARTTACNGCNGAAT 60				
AX958630		61 GTTGCTGCTTACGTTTCTAACCAAGCTGCTCTGTACTGAGCTTCTGCACTTATCT 120				
AX958630		61 GTNGCNGCTATGTTWMSAAVCAVGTNGTNCNGTNAANGARTMCCNGATNTATMSN 120				
AX958630		121 GATGTTCTACTGCACCTTTCTGGAACATCTGCTCTGCTTCTGTTGCTTTAAGTTAG 180				
AX958630		121 GAYGTCNCAVACNGCNYTWSNGNACNMSNGCNCNGMSGTNGCNGTNAAYGTNGAR 180				
AX958630		181 AAGCAGAGACCTGCTGTTCTGTTGCTGTAAGTCTGTTGAGATGATCATATGTTGTTG 240				
AX958630		181 AARCARARCCNGCNGTWSNGTNGNARMSGTNGARAGAYCAATATGTTGTTT 240				
AX958630		241 GAGTGTGCTGCTTCTTCAAGTCTCTCAAGGCTCACCTTACTCATCACTATGACT 300				
AX958630		241 GARTGYGNGGMSWSTTAAARNSVNTNABMGNCAYTNNACNACNCAVCAWMSNATGACN 300				
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AX958630		301 CCNGARGARATATYMGNGARAAARATGGGAYTTCNCGTNGATYTAACNATGGTNGCNCNGCN 360				
AX958630		361 TACGCTGAGGCTCGTCTCTCGTCTGCTGCTAGAGATGAGGCTCTCGGTCACCGTCTAAGGCT 420				
AX958630		361 TAYGNGNGRGCMGMSWNGNTNCCNARBARATGAGGAYTNGCNCARMMNGNBARCNCN 420				
AX958630		421 AACCGTCCAAAAAAGAGACGTAAAGT 446				
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AX958630	RESULT 5	AX963309				
AX958630	LOCUS	AX963309				
AX958630	ACCESSION	Sequence 3 from Patent WO03104462.				
AX958630	VERSION	AX963309.1				
AX958630	KEYWORDS	GI:40882062				
AX958630	SOURCE	.				
AX958630	ORGANISM	synthetic construct				
AX958630	REFERENCE	synthetic construct				
AX958630	AUTHORS	other sequences; artificial sequences.				
AX958630		1 Hannoufa, A., Lydiate, D. J. and Geo, M. J.				

TITLE		Regulation of gene expression using chromatin remodelling factors			
JOURNAL		Patent: WO 03104462-A 3 18-DEC-2003.			
		Her Majesty The Queen in Right of Canada, as represented; by The Minister of Agriculture and Agri-Food Canada (CA)			
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ORIGIN	misc_feature				
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	Best Local Similarity	58.3%;	Pred. No. 3.3e-86;		
	Matches .260;	Conservative 97;	Mismatches 89;	Indels 0;	Gaps 0;
QY	1	ATGACCTGAGACTGTTACGGTAAAGCTCAGAGATCTTGTGTGAGCTTACTGATATC	60		
Db	1	ATGCNCGARCCGNTATYGGAAAGCAGAGATYTTNGTNGARYTNAACNGCAGATAT	60		
QY	61	GTTCCTCTTACGTTTCTTACCAACGTTGTTCTGTACTGAGCTTCTGACTTATCT	120		
Db	61	GTNCNCGNTATYGTNNMAAYCAATGTTGCCNTNANCGARYTNCNGGNTATHTMSN	120		
QY	121	GAGTTGATACCTGACATTTCTGGAACATCTGCTCTTGCTTGTGCTTTAACGTTGAG	180		
Db	121	GAYTNCATYACNGGNTYTNMSGNAGACWMSGNCNCNMSGNTGNGCTTAAAGTNGAR	180		
QY	181	AAGCAGAAAGCTGCTGTTTCTGTTCCGTAAGTCTGTTGAGATGATCATTCGTTGTTG	240		
Db	181	AARCARAARCCNGCNGTNNMSGTMMGAARMSGNTNCARGAYGAYCAATHGTTGYTN	240		
QY	241	GAGTGTGGTGGTCTTCAAGTCTCTCAAGGTCACCTTACTACTCATCTACTGATGATC	300		
Db	241	GARTGTGNGNGNMTTYAARMSYTTAARAKNCAYTTNACNACNCAAYCAWSNATGACN	300		
QY	301	CCAGAGAGATATAGAGAAAGTGGGATCTTCTGTGTATTAACCTATGTTGCTCTGCT	360		
Db	301	CCNGARGARATYVNGARARATGGGAYTTCNCGTNCATYAYCCNATGGTNGCNCNGCN	360		
QY	361	TACCTGAAGCTCGTTTCTCGTCTGCTTAAGAGATGSGTCTCGGTACGCTCGTAAGCT	420		
Db	361	TAYCNCARGCNGMNMNMNGYTTNGCNAAARGATGGGNTGNCARMGNMGAARGCN	420		
QY	421	AACGCTCAAAAAAGACGTAAGCT	446		
Db	421	AAVGNCCNAARARARARMGNAARGT	446		
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LOCUS	AX685343	447 bp	DNA	linear	PAT 29-MAR-2003
DEFINITION	Sequence 3 from Patent W002095021.				
ACCESSION	AX685343				
VERSION	AX685343.1	GI:29371666			
KEYWORDS	.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	other sequences; artificial sequences.				
AUTHORS	1				
TITLE	Hannoufa, A., Hegedus, D. and Bate, N.				
JOURNAL	A repressor-mediated regulation system for control of gene expression in plants				
	Patent: WO 02095021-A 3 28-NOV-2002;				
	The Minister of Agriculture and Agri-Food Canada (CA)				
FEATURES	location/Qualifiers				
source	1. .447 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="ROS consensus sequence"				

ORIGIN

Query Match 69.2%; Score 317; DB 2; Length 447;
Best Local Similarity 58.3%; Pred. No. 3.3e-86;
Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACGGTAACGCTCAGAGATCTTCTGTTGAGCTTACTGCTGATATC 60
DB 1 ATGACNBARACNCGNTAYGNAAYGCNCARGAAYTNTGNTGNGARYTNACNGCNGAATH 60

QY 61 GTTGCTGCTTACGTTTCTTAACCAAGTGTTCCTGTTACTGAGCTTCTGCACTTATCTCT 120
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QY 121 GATGTCATACGACTTCTGGAACATCTGCTCTGCTCTCTGTTGCTGTTAAGTGGAG 180
DB 121 GATGTCNAYACNCGNTYTNMSNGNACNMSGNCNCGNMSNGTNGCNGTNAAYGTNGAR 180

QY 181 AAGCAGAAGCTGCTGTTTCTGTTCTGTAAGTCTGTTCAAGATGATCATTCGTTTGTG 240
DB 181 AACCARAARCCNCGNCGTNGTNGNAHMSNGTNCARGAAYCAVATHGTTNTGYTN 240

QY 241 GAGTGTGTGTTCTTCAAGTCTCTCAAGGCTCACTTACTACTCATCTATGACT 300
DB 241 GARTGCGNCGNMSNTTYAARMSYTNAAHMGNCAYYTNAACNCAVCAWMSNATGACN 300

QY 301 CCAGAGAGATATAGAGAAGTGGATCTTCTGTTGATTACCTATGATGTTGCTCTGCT 360
DB 301 CCGARBARATAYMNGNBARATGGAAYTNCNCGTNAAYATACNATGTCNCGNCGN 360

QY 361 TAGCTGAGGCTGTTCTGCTCTGCTTAAGAGATGGTCTCGTCAAGCTGTAAGCT 420
DB 361 TAYGNCNARCCNCGNMSNMGNTYTGCAARAGATGAGNTNGNCARMGNGMAARGCN 420

QY 421 AACCGTCAAAAAAGACGTTAAGT 446
DB 421 AATMGNCNARARARARARMGNAAGT 446

RESULT 7
LOCUS AX958628 429 bp DNA linear PAT 14-JAN-2004
DEFINITION Sequence 1 from Patent W003100063.
ACCESSION AX958628
VERSION AX958628.1 GI:40879468
KEYWORDS
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.

REFERENCE
AUTHORS Hamoufa, A., Hegedus, D. and Bate, N.
TITLE A repressor-mediated regulation system for control of gene
expression in plants
JOURNAL Patent: WO 03100063-A 1 04-DEC-2003;
Her Majesty The Queen in Right of Canada, as Represented; by The
Minister of Agriculture and Agri-Food (CA)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:358"

ORIGIN

Query Match 63.7%; Score 291.6; DB 2; Length 429;
Best Local Similarity 80.3%; Pred. No. 2.2e-78;
Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACGGTAACGCTCAGAGATCTTCTGTTGAGCTTACTGCTGATATC 60
DB 1 ATGACGAAACTGATACGGTAACGCCAGAGATCTGCTGTCGACACTGACGCGGATATT 60

QY 61 GTTGCTGCTTACGTTTCTTAACCAAGTGTTCCTGTTACTGAGCTTCTGCACTTATCTCT 120
DB 61 GTTGCGCTATGTTAGCAACCAAGTGTTCCTGTTACTGAGCTTCTGCGCTTATATTCG 120

QY 121 GATGTCATACGACTTCTGGAACATCTGCTCTGCTCTCTGTTGCTGTTAAGTGGAG 180
DB 121 GATGTCATACGCACTCAAGCGAACAATCGGACCGGATCGGTGGGCAATGTTGAA 180

QY 181 AAGCAGAAGCTGCTGTTTCTGTTCTGAAGTCTGTTCAAGATGATCATATCGTTTGTG 240
DB 181 AAGCAGAAGCTGCTGTTGTCGTTCCAGATGAGTCTCAGGACGATCATATCGTCTGTTG 240

QY 241 GAGTGTGTGTTCTTTCAAGTCTCTCAAGGCTCACTTACTATCATCATCTATGACT 300
DB 241 GATGTGTGCTGCTGTTCAAGTCTCAACGCGCACTGACGACATCAACAGATGACG 300

QY 301 CCAGAGAGATATAGAGAAGTGGATCTTCTGTTGATTACCTATGATGTTGCTCTGCT 360
DB 301 CCGAAGAAATATCGCAAAAATGGGATCTGCGGATGATTTATCCATGTTGCTCCGCC 360

QY 361 TAGCTGAGGCTGTTCTGCTCTGCTTAAGAGATGGTCTCGTCAAGCTGTAAGCT 420
DB 361 TAGCCGAAGCCGTTGCGGCTCGCCAAAGAAATGGTCTCGTCAAGGCGCGCAAGGCG 420

QY 421 AACCGT 426
DB 421 AACCGT 426

RESULT 8
LOCUS AX685341 429 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 1 from Patent W002095021.
ACCESSION AX685341
VERSION AX685341.1 GI:29371664
KEYWORDS
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.

REFERENCE
AUTHORS Hamoufa, A., Hegedus, D. and Bate, N.
TITLE A repressor-mediated regulation system for control of gene
expression in plants
JOURNAL Patent: WO 02095021-A 1 28-NOV-2002;
The Minister of Agriculture and Agri-Food Canada (CA)
FEATURES
source 1..429
/organism="Agrobacterium tumefaciens"
/mol_type="unassigned DNA"
/db_xref="taxon:358"

ORIGIN

Query Match 63.7%; Score 291.6; DB 2; Length 429;
Best Local Similarity 80.3%; Pred. No. 2.2e-78;
Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACGGTAACGCTCAGAGATCTTCTGTTGAGCTTACTGCTGATATC 60
DB 1 ATGACGAAACTGATACGGTAACGCCAGAGATCTGCTGTCGACACTGACGCGGATATT 60

QY 61 GTTGCTGCTTACGTTTCTTAACCAAGTGTTCCTGTTACTGAGCTTCTGCACTTATCTCT 120
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QY 181 AAGCAGAAGCTGCTGTTTCTGTTCTGAAGTCTGTTCAAGATGATCATATCGTTTGTG 240
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QY 241 GAGTGTGTGTTCTTTCAAGTCTCTCAAGGCTCACTTACTATCATCATCTATGACT 300
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DB 61 GTTGCTGCTTACGTTTCTTAACCAAGTGTTCCTGTTACTGAGCTTCTGCACTTATCTCT 120

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QY 421 AACCGT 426
DB 421 AACCGT 426

RESULT 8
LOCUS AX685341 429 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 1 from Patent W002095021.
ACCESSION AX685341
VERSION AX685341.1 GI:29371664
KEYWORDS
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.

REFERENCE
AUTHORS Hamoufa, A., Hegedus, D. and Bate, N.
TITLE A repressor-mediated regulation system for control of gene
expression in plants
JOURNAL Patent: WO 02095021-A 1 28-NOV-2002;
The Minister of Agriculture and Agri-Food Canada (CA)
FEATURES
source 1..429
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Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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DB 61 GTTGCGCTATGTTAGCAACCAAGTGTTCCTGTTACTGAGCTTCTGCGCTTATATTCG 120

QY 121 GATGTCATACGACTTCTGGAACATCTGCTCTGCTCTCTGTTGCTGTTAAGTGGAG 180
DB 121 GATGTCATACGCACTCAAGCGAACAATCGGACCGGATCGGTGGGCAATGTTGAA 180

QY 181 AAGCAGAAGCTGCTGTTTCTGTTCTGAAGTCTGTTCAAGATGATCATATCGTTTGTG 240
DB 181 AAGCAGAAGCTGCTGTTGTCGTTCCAGATGAGTCTCAGGACGATCATATCGTCTGTTG 240

QY 241 GAGTGTGTGTTCTTTCAAGTCTCTCAAGGCTCACTTACTATCATCATCTATGACT 300
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Matches 342; Conservative	0; Mismatches 84; Indels 0; Gaps 0;	
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QY	1 ATGACTAGAGACTGTTACGGTTAAAGCTCAGAGATCTTCTGTTGAGCTTAAGCTGATATC 60	
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QY	61 GTTCTGCTTACGTTTCTAACCAAGCTTCTGTTAATGAGCTTCTGACCTTATCTCT 120	
Db	369 GTGCTGCTATATTGACAAACACAGCTGTTCCGTAATGAGCTTCCGGCTTATTTTCG 428	
QY	121 GATGTTACTACTGACATTTCTGAAACATCTGCTCTCTCTCTGTTGCTTTAAGTTGAG 180	
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QY	181 AAGAGAAGACCTGCTGTTTCTGTCGTAAGCTGTTGAGATGATCATATGTTGTTTG 240	
Db	489 AAGAGAAGACCTGCTGTTGCTGTTGCTGTTGAGATGATCATATGTTGTTTG 548	
QY	241 GAGTGTGTTGTTTCTTCAAGCTCTCAAGGCTCACCTACTACTCATCATCTATGACT 300	
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QY	301 CCAGAGAGATTAAGAGAAAGTGGGATCTTCTGTTGATTAACCTATGTTGTTGCTCTGCT 360	
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QY	361 TAGCTGAGGCTGTTTCCGCTGCTGCTAAGAGATGGGCTCTCGGTCAAGCTGTAAGGCT 420	
Db	669 TAGCTGAGGCTGTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728	
QY	421 AACCGT 426	
Db	729 AACCGT 734	
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LOCUS	Agrobacterium tumefaciens str. C58	circular chromosome, section 80
DEFINITION	Agrobacterium tumefaciens str. C58	of 254 of the complete sequence.
ACCESSION	AE008022	AE007869
VERSION	AE008022.1	GI:15159900
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SOURCE		
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	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.	
REFERENCE	1 (bases 1 to 10212)	
AUTHORS	Hinkle,G., Slater,S.C. and Goodner,B.	
TITLE	Complete Genome Sequence of Agrobacterium tumefaciens C58 (Rhizobium radiobacter C58), the Causative Agent of Crown Gall Disease in Plants	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 10212)	
AUTHORS	Hinkle,G., Slater,S.C. and Goodner,B.	
TITLE	Direct Submission	
JOURNAL	Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street, Cambridge, MA 02139, USA	
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Query Match      59.3%; Score 271.4; DB 15; Length 10212;
Best Local Similarity 77.4%; Pred. No. 2.9e-72;
Matches 329; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTAAGGTAAGCCAGAGATCTTCTGTGAGCTTACTGCGATATC 60
Db 7656 ATGACGGAAGCTGATAGGTAAGCCAGAGATCTGCTGCGAAGTGAAGCGGAGATAT 7715
QY 61 GTTGCTCTTACGTTTCTTAAACAAGTTGTTCTGTACTGAGCTTCTGACCTATCTCT 120
Db 7716 GTTGCTCTTACGTTTCTTAAACAAGTTGTTCTGTACTGAGCTTCTGACCTATCTCT 7775
QY 121 GATGTCATCTGACATTTCTGGAACATCTGCTCTCTGCTTGTGCTTTAAGCTTGA 180
Db 7776 GATGTCATCTGACATTTCTGGAACATCTGCTCTCTGCTTGTGCTTTAAGCTTGA 7835
QY 181 AAGGAGAGCGTCTGCTTCTGTCGTAAGCTGTCGTAAGATGATCATTCGTTGTTG 240
Db 7836 AAGGAGAGCGTCTGCTTCTGTCGTAAGCTGTCGTAAGATGATCATTCGTTGTTG 7895
QY 241 GAGTGTGCTGTTCTTCAAGTCTCTCAAGCGTACCTTACTACTCATCTATGACT 300
Db 7896 GAGTGTGCTGTTCTTCAAGTCTCTCAAGCGTACCTTACTACTCATCTATGACT 7955
QY 301 CCAGAGAGATVAGAGAAAGTGGATCTTCTGTGATTAACCTATGTTGCTCTGCT 360
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QY 361 TAGCGTAGGCTGCTTCTGCTCTGCTAAGAGATGCTCGGTCAGCGTCTGAAGCT 420
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QY 421 AACCG 425
Db 8076 AGCCG 8080

RESULT 11
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LOCUS Agrobacterium tumefaciens str. C58 circular chromosome, section 82
DEFINITION Agrobacterium tumefaciens str. C58 circular chromosome, section 82
ACCESSION AE009056 AE008688
VERSION AE009056.1 GI:17739283
KEYWORDS
SOURCE Agrobacterium tumefaciens str. C58
ORGANISM Agrobacterium tumefaciens str. C58

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REFERENCE
AUTHORS
Wood,D.W., Setubal,J.C., Kaul,R., Monks,D., Chen,L., Wood,G.E.,
1 (bases 1 to 10229)
Chen,Y., Woo,L., Kitejima,J.P., Okura,V.K., Almeida,N.F., Jr.,
Zhou,Y., Boyee,D., Sr., Chapman,P., Clendenning,J., Deatherage,G.,
Gillet,W., Grant,C., Guenther,D., Kutyavin,T., Levy,R., Li,M.,
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Karp,P., Romero,P., Zhang,S., Yoo,H., Tao,Y., Biddle,P., Jung,M.,
Krespan,W., Perry,M., Gordon-Kamm,B., Liao,L., Kim,S., Hendrick,C.,
Zhao,Z., Dolan,M., Tingey,S.V., Tomb,J., Gordon,M.P., Olson,M.V.,
and Nester,E.W.
The genome of the natural genetic engineer Agrobacterium
tumefaciens C58
Science 294 (5550) , 2317-2323 (2001)
11743193
JOURNAL
PUBMED
2 (bases 1 to 10229)
11743193
AUTHORS
Chen,Y., Woo,L., Kitejima,J.P., Okura,V.K., Almeida,N.F., Jr.,
Zhou,Y., Boyee,D., Sr., Chapman,P., Clendenning,J., Deatherage,G.,
Gillet,W., Grant,C., Guenther,D., Kutyavin,T., Levy,R., Li,M.,
McClelland,E., Palmieri,A., Raymond,C., Rouse,G.,
Saenphimmachak,C., Wu,Z., Gordon,D., Eisen,J.A., Paulsen,I.,
Karp,P., Romero,P., Zhang,S., Yoo,H., Tao,Y., Biddle,P., Jung,M.,
Krespan,W., Perry,M., Gordon-Kamm,B., Liao,L., Kim,S., Hendrick,C.,
Zhao,Z., Dolan,M., Tingey,S.V., Tomb,J., Gordon,M.P., Olson,M.V.,
and Nester,E.W.
Submitted (27-SEP-2001) Department of Microbiology, University of
Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
98195-7242, USA
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Query Match 59.3%; Score 271.4; DB 15; Length 10229;
Best Local Similarity 77.4%; Pred. No. 2,9e-72;
Matches 329; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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ACCESSION X82941
VERSION   X82941.1 GI:599612
KEYWORDS   ros gene.
SOURCE     Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM   Agrobacterium tumefaciens (Rhizobium radiobacter);
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REFERENCE 1
AUTHORS   Brightwell,G., Hussain,H., Tiburtius,A., Yeoman,K.H. and
            Johnston,A.W.
TITLE      Pleiotropic effects of regulatory ros mutants of Agrobacterium
            radiobacter and their interaction with Fe and glucose
            Mol. Plant Microbe Interact. 8 (5), 747-754 (1995)
JOURNAL   7579618
REFERENCE 2 (bases 1 to 783)
AUTHORS   Hussain,H.A.
TITLE      Direct Submission
            Submitted (28-NOV-1994) H.A. Hussain, University of East Anglia,
            School of Biological Sciences, Norwich NR4 7TU, UK
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ORIGIN
Query Match 59.0%; Score 270; DB 15; Length 783;
Best Local Similarity 76.0%; Pred. No. 9.5e-72;
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ACCESSION AY683454
VERSION   AY683454.1 GI:51012475
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SOURCE     Rhizobium leguminosarum bv. trifolii
            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
            Rhizobiaceae; Rhizobium.
REFERENCE 1 (bases 1 to 856)
AUTHORS   Janczarek,M.B. and Skorupska,A.
TITLE      rostr gene of Rhizobium leguminosarum bv. trifolii influencing on
            the exopolysaccharide production
            unpublished
JOURNAL   2 (bases 1 to 856)
REFERENCE 2
AUTHORS   Janczarek,M.B. and Skorupska,A.
TITLE      Direct Submission
            Submitted (12-JUL-2004) General Microbiology, M. Curie-Sklodowska
            University, Akademicka 19, Lublin 20-033, Poland
FEATURES
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            /mol_type="genomic DNA"
            /strain="TAL"
            /db_xref="taxon:386"
            /note="biovar: trifolii"
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            /gene="rostr"
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            /gene="rostr"
            CDS
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            /gene="rostr"
            /note="DNA binding protein; similar to Rhizobium etl1
            RosR, Agrobacterium tumefaciens Ros and Sinorhizobium
            meliloti Muck; regulator of exopolysaccharide synthesis;
            member of Ros/MucR family of transcriptional regulators"
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            /db_xref="GI:51012476"
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            ALSNTSVPQAAIIVEKQPAVSVRKSDVDHIVCLECGNFKSLRHLMTTHSLSPB
            EYREKMDLPDYPMVAPAVAEARSRLAKEMGLGRRKRRG"

ORIGIN
Query Match 46.3%; Score 212.2; DB 15; Length 856;

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 22:31:06 ; Search time 484 Seconds
(without alignments)
6597.706 Million cell updates/sec

Title: US-10-719-996A-2

Sequence: 1 atgactgcgaactgcgtacg9.....cgtacagctcgcagactcgc 458

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	458	100.0	458	8	AAD52861
2	458	100.0	458	12	AAL56364
3	458	100.0	472	8	AAD52884
4	458	100.0	472	12	AD114224
5	458	100.0	472	12	ADR22387
6	317	69.2	447	8	AAD52862
7	317	69.2	447	12	AD114225
8	317	69.2	447	12	AAL56365
9	291.6	63.7	429	8	AAD52860
10	291.6	63.7	429	12	AAL56363
11	291.6	63.7	429	12	ADR22405
12	199.4	43.5	110000	2	AAV30458_0
13	199.4	43.5	110000	2	AAV30458_3
14	94.4	20.6	110000	2	AAV30459_3
15	94.4	20.6	110000	2	AAV30459_3
16	68	14.8	486	4	AAV75507
17	64	14.0	3489	3	AAA30290
18	64	14.0	3489	4	AAV82901

C 19	64	14.0	3489	6	ABA93487	ABA93487 Kaposi's
C 20	64	14.0	3489	12	AD165095	AD165095 HIV8 DNA
C 21	64	14.0	3489	14	ADV68153	ADV68153 Kaposi's
C 22	64	14.0	32207	2	AAV73805	AAV73805 KSHV LTR
C 23	64	14.0	137507	2	AAV19941	AAV19941 KSHV long
C 24	64	14.0	137508	12	ADN12162	ADN12162 Human her
C 25	61	13.3	408	12	ADN97264	ADN97264 AGC10 loc
C 26	61	13.3	408	12	ADN97258	ADN97258 AGC10 STR
C 27	61	13.3	408	12	ADN97265	ADN97265 AGC10 rev
C 28	59.2	12.9	204803	12	ADQ97348	ADQ97348 Mouse can
C 29	58.8	12.8	3499	12	ADQ67296	ADQ67296 Novel hum
C 30	58.2	12.7	6558	12	AAZ45602	AAZ45602 cDNA sequ
C 31	57.8	12.6	213	12	ADQ97263	ADQ97263 AGC10 arr
C 32	57.6	12.6	439	4	AA122718	AA122718 Probe #12
C 33	57.6	12.6	439	4	ABA67796	ABA67796 Human toe
C 34	57.6	12.6	439	4	AA148016	AA148016 Probe #16
C 35	57.6	12.6	439	4	ABA49878	ABA49878 Human bre
C 36	57.6	12.6	439	6	ABA34854	ABA34854 Probe #13
C 37	57.6	12.6	439	4	AAK41953	AAK41953 Human bon
C 38	57.6	12.6	439	4	AAK16207	AAK16207 Human bra
C 39	57.6	12.6	439	4	ABSA1558	ABSA1558 Human liv
C 40	57.6	12.6	439	5	AA108383	AA108383 Probe #83
C 41	57.6	12.6	439	6	ABSA15980	ABSA15980 Human gen
C 42	57.4	12.5	3150	6	ABZ12438	ABZ12438 Arabidops
C 43	57.4	12.5	4283	13	ADX31923	ADX31923 plant full
C 44	57.2	12.5	2614	6	ABK36100	ABK36100 cDNA sequ
C 45	57.2	12.5	6604	6	ABN95250	ABN95250 Gene #174

ALIGNMENTS

RESULT 1	
ID : AAD52861 standard; DNA; 458 BP.	
AA52861	
AC AAD52861;	
DT 14-MAY-2003 (first entry)	
XX Agrobacterium tumefaciens ros repressor codon optimised DNA #1.	
DE Agrobacterium tumefaciens ros repressor codon optimised DNA #1.	
XX ROS repressor protein; gene expression; ds.	
OS Agrobacterium tumefaciens.	
OS Synthetic.	
PN WO200295021-A2.	
XX 28-NOV-2002.	
PD 23-MAY-2002; 2002WO-CA000740.	
PF 23-MAY-2001; 2001US-0292973P.	
XX (MIAC) CANADA DEPT AGRIC & AGRI-FOOD CANADA.	
PA Hamoufa A, Hegedus D, Bate N;	
XX WPI; 2003-148467/14.	
DR New nucleic acid molecule encoding a ROS repressor, useful for	
XX controlling gene expression in plants, comprises a regulatory region	
PT operatively linked to a gene of interest and one or more ROS operator	
PT sequence.	
XX Claim 2; Page 70; 84pp; English.	
PS The present invention relates to a novel nucleic acid molecule encoding a	
XX ROS repressor protein optimised for plant codon usage and exhibiting ROS	
CC operator binding activity and/or ROS repressor activity. The nucleic acid	
CC molecule comprises a regulatory region operatively linked to a gene of	
CC interest and one or more ROS operator sequence capable of controlling the	

CC activity of the regulatory region that is functional in plants. They are
 CC useful in controlling gene expression in plants using a repressor protein
 CC and corresponding operator sequences. The present sequence is
 CC Agrobacterium tumefaciens ros repressor codon optimised DNA

XX Sequence 458 BP; 91 A; 105 C; 111 G; 151 T; 0 U; 0 Other;

Query Match 100.0%; Score 458; DB 8; Length 458;
 Best Local Similarity 100.0%; Pred. No. 2,7e-121;
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTAACGTAACGCTCAGAGATCTTTGTTGAGCTTACTGCTGATATC 60
 Db 1 ATGACTGAGACTGCTTAACGTAACGCTCAGAGATCTTTGTTGAGCTTACTGCTGATATC 60
 QY 61 GTTGCTGCTTAACGTTTAAACGATGTTGCTTCTTACTGAGCTTCTGGAATTATCTCT 120
 Db 61 GTTGCTGCTTAACGTTTAAACGATGTTGCTTCTTACTGAGCTTCTGGAATTATCTCT 120
 QY 121 GATGTCATATGACTGCTTCTGGAACATCTGCTCTGCTTCTGTTGCTTTAAGCTTGAG 180
 Db 121 GATGTCATATGACTGCTTCTGGAACATCTGCTCTGCTTCTGTTGCTTTAAGCTTGAG 180
 QY 181 AAGCAGAAAGCTGCTGTTTCTGTTGCTGAAGTCTGTTGAGATGATCATATGTTGTTTG 240
 Db 181 AAGCAGAAAGCTGCTGTTTCTGTTGCTGAAGTCTGTTGAGATGATCATATGTTGTTTG 240
 QY 241 GAGGTGCTGCTTCTTCAAGTCTCAAGGCTACCTTACTACTACTACTACTACTACTACT 300
 Db 241 GAGGTGCTGCTTCTTCAAGTCTCAAGGCTACCTTACTACTACTACTACTACTACTACT 300
 QY 301 CCAAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATAGTGTGCTCTGCT 360
 Db 301 CCAAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATAGTGTGCTCTGCT 360
 QY 361 TACGCTGAGGCTCGTTCTCGTCTGCTTAAGAGATGGGCTCGGTCAAGCTGTAAGGCT 420
 Db 361 TACGCTGAGGCTCGTTCTCGTCTGCTTAAGAGATGGGCTCGGTCAAGCTGTAAGGCT 420
 QY 421 AACCGTCAAAAAGAAAGCGTAAGGCTGAGAGCTGCC 458
 Db 421 AACCGTCAAAAAGAAAGCGTAAGGCTGAGAGCTGCC 458

RESULT 2

AA156364 standard; DNA; 458 BP.

XX AA156364;

XX 22-APR-2004 (first entry)

XX ROS gene repressor sequence.

XX Gene expression system; plant; ROS; vector; metabolic engineering; gene;
 XX ds.

XX Undentified.

XX WO2003100063-A1.

XX 04-DEC-2003.

XX 21-NOV-2002; 2002WO-CA001807.

XX 23-MAY-2002; 2002WO-CA000740.

XX (MIAC) CANADA MIN AGRIC & AGRI-FOOD.

XX Hannoufa A, Hegedue D, Bate N;

XX WPI; 2004-035150/03.

PT New nucleic acids encoding a ROS repressor optimized for plant codon
 PT usage and exhibits ROS operator binding activity. ROS repressor activity
 PT or both, useful for regulating gene expression in plants.

XX Claim 2; Page 91; 0pp; English.

XX The present invention relates to a nucleic acid construct comprising a
 CC regulatory region operatively linked to a gene of interest and one or
 CC more ROS operator sequence capable of controlling the activity of the
 CC regulatory region which is functional in plants, encodes a ROS repressor
 CC optimised for plant codon usage and exhibits ROS operator binding
 CC activity. ROS repressor activity or both. The nucleic acid molecule or
 CC its derivative is useful for the regulation of gene expression in plants.
 CC The gene expression can be used in metabolic engineering to produce
 CC plants that accumulate large amounts of certain intermediate compounds.
 CC The present sequence is a polynucleotide used in constructs of the
 CC invention

XX Sequence 458 BP; 91 A; 105 C; 111 G; 151 T; 0 U; 0 Other;

Query Match 100.0%; Score 458; DB 12; Length 458;
 Best Local Similarity 100.0%; Pred. No. 2,7e-121;
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTAACGTAACGCTCAGAGATCTTTGTTGAGCTTACTGCTGATATC 60
 Db 1 ATGACTGAGACTGCTTAACGTAACGCTCAGAGATCTTTGTTGAGCTTACTGCTGATATC 60
 QY 61 GTTGCTGCTTAACGTTTAAACGATGTTGCTTCTTACTGAGCTTCTGGAATTATCTCT 120
 Db 61 GTTGCTGCTTAACGTTTAAACGATGTTGCTTCTTACTGAGCTTCTGGAATTATCTCT 120
 QY 121 GATGTCATATGACTGCTTCTGGAACATCTGCTCTGCTTCTGTTGCTTTAAGCTTGAG 180
 Db 121 GATGTCATATGACTGCTTCTGGAACATCTGCTCTGCTTCTGTTGCTTTAAGCTTGAG 180
 QY 181 AAGCAGAAAGCTGCTGTTTCTGTTGCTGAAGTCTGTTGAGATGATCATATGTTGTTTG 240
 Db 181 AAGCAGAAAGCTGCTGTTTCTGTTGCTGAAGTCTGTTGAGATGATCATATGTTGTTTG 240
 QY 241 GAGGTGCTGCTTCTTCAAGTCTCAAGGCTACCTTACTACTACTACTACTACTACTACT 300
 Db 241 GAGGTGCTGCTTCTTCAAGTCTCAAGGCTACCTTACTACTACTACTACTACTACTACT 300
 QY 301 CCAAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATAGTGTGCTCTGCT 360
 Db 301 CCAAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATAGTGTGCTCTGCT 360
 QY 361 TACGCTGAGGCTCGTTCTCGTCTGCTTAAGAGATGGGCTCGGTCAAGCTGTAAGGCT 420
 Db 361 TACGCTGAGGCTCGTTCTCGTCTGCTTAAGAGATGGGCTCGGTCAAGCTGTAAGGCT 420
 QY 421 AACCGTCAAAAAGAAAGCGTAAGGCTGAGAGCTGCC 458
 Db 421 AACCGTCAAAAAGAAAGCGTAAGGCTGAGAGCTGCC 458

RESULT 3

AA52884 standard; DNA; 472 BP.

XX AA52884;

XX 14-MAY-2003 (first entry)

XX Agrobacterium tumefaciens ros repressor codon optimised DNA #2.

XX ROS repressor protein; gene expression; ds.

XX Agrobacterium tumefaciens.

XX Key Location/Qualifiers

XX misc_feature 442

[illegible]

Query	Match	Score	DB 12	Length	472
Best Local Similarity	100.0%	Score 458	DB 12	Length 472	
Matches 458	Conservative 0	Mismatches 0	Indels 0	Gaps 0	

Query	Match	Score	DB 12	Length	472
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15	ATGACTGAGACTGCTTACGCGTAAGCGTCGATCTCTTGAGCTTACGCTATGC	74			

QY 61 GTTGCTGCTTACGTTTCTAAACGAGTGTTCCTGTTACTAGAGCTTCTGAGCTTATCTCT 120
 DB 75 GTTGCTGCTTACGTTTCTAAACGAGTGTTCCTGTTACTAGAGCTTCTGAGCTTATCTCT 134
 QY 121 GATGTTCAATCTGACCTTTCTGGAACATCTGCTCTGCTTCTGTTGCTTTAAAGTTGAG 180
 DB 135 GATGTTCAATCTGACCTTTCTGGAACATCTGCTCTGCTTCTGTTGCTTTAAAGTTGAG 194
 QY 181 AACGAGAAAGCTGCTGTTTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTG 240
 DB 195 AACGAGAAAGCTGCTGTTTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTG 254
 QY 241 GAGTGTGTGTTCTTCTTCAAGTCTCTCAAGCTCACTTACTATCACTATCACTATGACT 300
 DB 255 GAGTGTGTGTTCTTCTTCAAGTCTCTCAAGCTCACTTACTATCACTATCACTATGACT 314
 QY 301 CCAGAGAGATATAGAGAGAGTGGATCTTCTGTTATTAACCTATAGTTGCTCTGCT 360
 DB 315 CCAGAGAGATATAGAGAGAGTGGATCTTCTGTTATTAACCTATAGTTGCTCTGCT 374
 QY 361 TAGGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCGGCTCAGCGTGGTAAAGCT 420
 DB 375 TAGGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCGGCTCAGCGTGGTAAAGCT 434
 QY 421 AACCGTCCAAAAAAGAACGCTAAGTCTGAGAGCTCGC 458
 DB 435 AACCGTCCAAAAAAGAACGCTAAGTCTGAGAGCTCGC 472

RESULT 5
 ID ADR22387 standard; DNA; 472 BP.
 AC ADR22387;

DT 07-OCT-2004 (first entry)
 XX Agrobacterium tumefaciens plant-optimised Ros selectable marker DNA.
 DE Agrobacterium tumefaciens plant-optimised Ros selectable marker DNA.
 XX Agrobacterium tumefaciens plant-optimised Ros selectable marker DNA.
 KM Agrobacterium tumefaciens plant-optimised Ros selectable marker DNA.
 XX Agrobacterium tumefaciens plant-optimised Ros selectable marker DNA.
 OS Agrobacterium tumefaciens plant-optimised Ros selectable marker DNA.
 XX Agrobacterium tumefaciens plant-optimised Ros selectable marker DNA.
 FH Key Location/Qualifiers
 FT 15..464
 FT /tag= a
 FT /product= "Agrobacterium tumefaciens plant-optimised Ros
 FT selectable marker protein"

CA2442521-A1.
 PD 03-APR-2004.
 XX 03-OCT-2003; 2003CA-02442521.
 PF 03-OCT-2002; 2002US-0416369P.
 XX 03-OCT-2002; 2002US-0416369P.
 PA (MIAC) CANADA MIN AGRICULTURE.
 XX Hegedus D, Bate N, Hamoufa A, Lydiate D;
 DR WPI: 2004-341154/32.
 XX P-PSDB; ADR22389.

PT Repressor-mediated plant selection strategies to identify transgenic
 PT plants comprising using a selectable marker system for plant
 PT transformation that is benign to the plant and confers no advantage to
 PT other organisms after gene transfer.
 XX Example 2; SEQ ID NO 1; 125pp; English.

CC The invention relates to novel repressor-mediated plant selection
 CC strategies to identify and select plants, cells, tissue or entire plants
 CC which comprise a coding region of interest. The methods of the invention
 CC may be used for selecting transgenic plants, cells, tissue or entire
 CC plants which comprise a coding region of interest. The methods are not
 CC based on antibiotic resistance, are simple to carry out and provide a
 CC selectable marker system for plant transformation that is benign to the
 CC transformed plant and confers no advantage to other organisms in the
 CC event of gene transfer. The methods involve stringent selection of
 CC transformed cells and use an inexpensive and effective selection agent
 CC that is non-toxic to plant cells. The current sequence is that of the
 CC Agrobacterium tumefaciens plant-optimised Ros selectable marker DNA of
 CC the invention.

SO Sequence 472 BP; 92 A; 110 C; 117 G; 153 T; 0 U; 0 Other;
 Query Match 100.0%; Score 458; DB 12; Length 472;
 Best Local Similarity 100.0%; Pred. No. 2.7e-121;
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACGCTAAGCTCAGAGATCTTCTGTTAGCTTACTGCTATATC 60
 DB 15 ATGACTGAGACTGCTTACGCTAAGCTCAGAGATCTTCTGTTAGCTTACTGCTATATC 74
 QY 61 GTTGCTGCTTACGTTTCTAAACGAGTGTTCCTGTTACTAGAGCTTCTGAGCTTATCTCT 120
 DB 75 GTTGCTGCTTACGTTTCTAAACGAGTGTTCCTGTTACTAGAGCTTCTGAGCTTATCTCT 134
 QY 121 GATGTTCAATCTGACCTTTCTGGAACATCTGCTCTGCTTCTGTTGCTTTAAAGTTGAG 180
 DB 135 GATGTTCAATCTGACCTTTCTGGAACATCTGCTCTGCTTCTGTTGCTTTAAAGTTGAG 194
 QY 181 AACGAGAAAGCTGCTGTTTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTG 240
 DB 195 AACGAGAAAGCTGCTGTTTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTG 254
 QY 241 GAGTGTGTGTTCTTCTTCAAGTCTCTCAAGCTCACTTACTATCACTATCACTATGACT 300
 DB 255 GAGTGTGTGTTCTTCTTCAAGTCTCTCAAGCTCACTTACTATCACTATCACTATGACT 314
 QY 301 CCAGAGAGATATAGAGAGAGTGGATCTTCTGTTATTAACCTATAGTTGCTCTGCT 360
 DB 315 CCAGAGAGATATAGAGAGAGTGGATCTTCTGTTATTAACCTATAGTTGCTCTGCT 374
 QY 361 TAGGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCGGCTCAGCGTGGTAAAGCT 420
 DB 375 TAGGCTGAGGCTGCTTCTGCTCTGCTAAGAGATGGGCTCGGCTCAGCGTGGTAAAGCT 434
 QY 421 AACCGTCCAAAAAAGAACGCTAAGTCTGAGAGCTCGC 458
 DB 435 AACCGTCCAAAAAAGAACGCTAAGTCTGAGAGCTCGC 472

RESULT 6
 ID AAD52862 standard; DNA; 447 BP.
 AC AAD52862;
 DT 14-MAY-2003 (first entry)

XX Agrobacterium tumefaciens ros repressor consensus DNA.
 DE Agrobacterium tumefaciens ros repressor consensus DNA.
 XX Agrobacterium tumefaciens ros repressor consensus DNA.
 KM Agrobacterium tumefaciens ros repressor consensus DNA.
 OS Agrobacterium tumefaciens ros repressor consensus DNA.
 XX Agrobacterium tumefaciens ros repressor consensus DNA.

PT Repressor-mediated plant selection strategies to identify transgenic
 PT plants comprising using a selectable marker system for plant
 PT transformation that is benign to the plant and confers no advantage to
 PT other organisms after gene transfer.
 XX Example 2; SEQ ID NO 1; 125pp; English.

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FT	/*tag= d
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FT	76. .78
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FT	103. .105
FT	/*tag= f
FT	/note= "Encodes Leu"
FT	112. .114
FT	/*tag= g
FT	/note= "Encodes Leu"
FT	118. .120
FT	/*tag= h
FT	/note= "Encodes Ser"
FT	136. .138
FT	/*tag= i
FT	/note= "Encodes Leu"
FT	139. .141
FT	/*tag= j
FT	/note= "Encodes Ser"
FT	148. .150
FT	/*tag= k
FT	/note= "Encodes Ser"
FT	160. .162
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FT	/*tag= m
FT	/note= "Encodes Ser"
FT	205. .207
FT	/*tag= n
FT	/note= "Encodes Arg"
FT	211. .213
FT	/*tag= o
FT	/note= "Encodes Ser"
FT	238. .240
FT	/*tag= p
FT	/note= "Encodes Leu"
FT	253. .255
FT	/*tag= q
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FT	313. .315
FT	/*tag= w
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FT	328. .330
FT	/*tag= x
FT	/note= "Encodes Leu"
FT	373. .375
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FT	376. .378
FT	/*tag= z
FT	/note= "Encodes Ser"

Query Match	Best Local Similarity	Score	31.7;	DB	8;	Length	447;		
Matches	260;	Conservative	97;	Mismatches	89;	Indels	0;	Gaps	0
1	ATGACTGAGCTGCTTACCGTAAACGCTGAGATCTTCTGTTGAGCTTACTGCTGATATC	60							
1	ATGACNGARACNGCNTATAGNAAYGCNARAGYYTNTGNTNGARYYTNAACNGCAGAYATH	60							
61	GTGTGCTTACGTTTCTTAAACGAGTTGTTCTGTTACTAGAGCTTCTGGAAGTATCTCT	120							
61	GTGNGCNGCNTATGTTWNSNAAYCAVGTGNTGNCNGTNAACNGARYYTNCNGGAYTNAATHWSN	120							
121	GATGTGCTTACGCTTCTGGAACATCTGCTGCTTCTGTTGCTGTTAGCTTAAAGTTAG	180							
121	GAYGTNCAVYACNGCNYTWMNSNGNACNWSNCCNGCNSNGTNGCNGTNAAYGTNGAR	180							
181	AAGCAGAAGCTGCTGTTCTGTTGTAAGCTGTTCAGAGTATCATATCGTTTGTG	240							

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Db      181 AACARARARCCGNGNMTNMGNAARMSNCTNCARAGYGAATGHTGTYTN 240
Qy      241 GAGGTGTGTTCTTTCAAGTCTCTCAAGGCTACCTTACTACTATGACT 300
Db      241 GARTGNGNMGNSMTTYAARMNSNYTNAARMNCAYTTNACNCAVCYMSNATACN 300
Qy      301 CCAGAGAGTATAGAGAAAGTGGATCTTCTGTTATTAACCTTAGTGTGCTGCT 360
Db      301 CCGARARARATYMGNGARARATGGATYTTNCCNGTNGATYATCCNATGNTGNCNCGN 360
Qy      361 TAGGCTGAGGCTGCTTCTGCTGCTAAGAGATGGGCTCGGTCAAGCTGTAAGCT 420
Db      361 TAYGCGNGARCGNMGNSMGTNYTNGCNAARARATGGGNTYNGNCARMGNGNAARCN 420
Qy      421 AACCGTCCAAAAAGAACGCTAAGCT 446
Db      421 AAYMNCNNAARARARARMGNAARGT 446

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RESULT 7

```

AD114225
ID      AD114225 standard; DNA; 447 BP.
XX
AC      AD114225;
XX
DT      22-APR-2004 (first entry)
XX
DE      Plant codon optimised degenerate A_tumefaciens ROS DNA SeqID 3.
XX

```

ROS; ds; transgenic plant; chromatin remodeling factor;
DNA binding protein; VP16; GAL4; recruitment factor; BnSCL1; bnRCP1;
histone acetyl transferase; HAT; histone deacetylase; HD; HDA; HDAC;
HDA19; cold tolerance.

Agrobacterium tumefaciens.
Synthetic.

MO2003104462-A2.

18-DEC-2003.

06-JUN-2003; 2003MO-CA000822.

06-JUN-2002; 2002US-0387088P.

(MIAC) CANADA DEPT AGRIC & AGRI-FOOD CANADA.

Hannoufa A, Lydiata DJ, Gao M;

WPI; 2004-062364/06.

Regulating expression of a nucleic acid sequence of interest by providing
a eukaryote and growing the eukaryote.

Disclosure; SEQ ID NO 3; 178pp; English.

This invention relates to a novel method for regulating gene expression
in transgenic plants using chromatin remodeling factors. Specifically,
it comprises transforming a plant with one or more constructs comprising
a first nucleotide sequence that is operably linked to a regulatory
region and is capable of binding to a fusion protein, and a second
nucleotide sequence that encodes said fusion protein. This fusion protein
comprises a DNA binding protein (VP16 or GAL4) or a portion thereof,
that can bind to and regulate expression of the gene of interest (i.e.,
the first polynucleotide) and a recruitment factor protein (BnSCL1 or
bnRCP1) that can bind to a chromatin remodeling protein. The present
invention describes the chromatin remodeling protein as a histone acetyl
transferase (HAT) or histone deacetylase (referred to as either HD, HDA
or HDAC), which is used to alter the structure of chromatin,
preferably this protein is HDA19. As such, this method can be used to
alter plant characteristics and phenotype e.g. to increase cold tolerance
by regulating the expression of a nucleic acid sequence of interest. This

CC polynucleotide sequence is the degenerate Agrobacterium tumefaciens ROS
CC DNA sequence codon optimised for use in plants, used in an
CC exemplification of the invention.

XX Sequence 447 BP; 80 A; 53 C; 81 G; 46 T; 0 U; 187 Other;

Query Match 69.2%; Score 317; DB 12; Length 447;

Best local Similarity 58.3%; Pred. No. 9e-81;

Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;

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Qy      1 ATGACTGAGACTGCTTAACGCTCAAGATCTTCTGTTAGCTTACTGCTGATATC 60
Db      1 ATGACNGARACNCGNCTAYGGNAAYGCNCARGAYTTTGTGTGATRYTNAACNCGNGAYATH 60
Qy      61 GTTGCTGCTTACGCTTCTAACACAGTTGTTCCGTTACTGAGCTTCTGACTTATCT 120
Db      61 GTNGCNGCNTAYGTMNSNAAVCAYGTNGTNCNGTACNGARITTCNGGNTYTNATHMSN 120
Qy      121 GATGTTCACTACTGCACTTCTGGAACATCTGCTGCTTCTGTTGCTTTAAGTTGAG 180
Db      121 GAYGTNCAYACNCGNCTNTMNSNGNACNMSNGCNCNCGNCSNGTNGCNATNAAYGTNGAR 180
Qy      181 AAGCAGAAGCTGCTGTTTCTGTTCTGTTAGTCTGTTCAAGATGATCATATCGTTGTTG 240
Db      181 AACARARARCCNCGNMTNMGNSMTTYAARMNSNYTNAARMNCAYTTNACNCAVCYMSNATACN 240
Qy      241 GAGGTGTGTTCTTCAAGTCTCTCAAGGCTGACCTTACTCTCATCTCATCTATGACT 300
Db      241 GARTGNGNMGNSMTTYAARMNSNYTNAARMNCAYTTNACNCAVCYMSNATACN 300
Qy      301 CCAGAGAGTATAGAGAAAGTGGATCTTCTGTTATTAACCTTAGTGTGCTGCTGCT 360
Db      301 CCGARARARATYMGNGARARATGGATYTTNCCNGTNGATYATCCNATGNTGNCNCGN 360
Qy      361 TAGGCTGAGGCTGCTTCTGCTGCTAAGAGATGGGCTCGGTCAAGCTGTAAGCT 420
Db      361 TAYGCGNGARCGNMGNSMGTNYTNGCNAARARATGGGNTYNGNCARMGNGNAARCN 420
Qy      421 AACCGTCCAAAAAGAACGCTAAGCT 446
Db      421 AAYMNCNNAARARARARMGNAARGT 446

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RESULT 8

AD156365

AD156365; standard; DNA; 447 BP.

22-APR-2004 (first entry)

ROS gene consensus sequence.

Gene expression system; plant; ROS; vector; metabolic engineering; gene;
ds.

Unidentified.

MO2003100063-A1.

04-DEC-2003.

21-NOV-2002; 2002MO-CA001807.

23-MAY-2002; 2002MO-CA000740.

(MIAC) CANADA MIN AGRIC & AGRI-FOOD.

Hannoufa A, Hegedus D, Bate N;

WPI; 2004-035150/03.

New nucleic acids encoding a ROS repressor optimized for plant codon

PT usage and exhibits ROS operator binding activity, ROS repressor activity
PT or both, useful for regulating gene expression in plants.

PS Claim 25; Page 93; Opp; English.

CC The present invention relates to a nucleic acid construct comprising a
CC regulatory region operatively linked to a gene of interest and one or
CC more ROS operator sequence capable of controlling the activity of the
CC regulatory region which is functional in plants, encodes a ROS repressor
CC optimised for plant codon usage and exhibits ROS operator binding
CC activity, ROS repressor activity or both. The nucleic acid molecule or
CC its derivative is useful for the regulation of gene expression in plants
CC The gene expression can be used in metabolic engineering to produce
CC plants that accumulate large amounts of certain intermediate compounds.
CC The present sequence is a polynucleotide used in constructs of the
CC invention

Sequence 447 BP; 80 A; 53 C; 81 G; 46 T; 0 U; 187 Other;

Query Match	Score	DB	Length
69.2%;	317;	12;	447;
Best Local Similarity	58.2%;	Prod No	90-81;

Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;

Qy	1	ATACCTAGAGCTGCTTACCGGTAAACGCTCAGATCTTCTGTTGAGCTTACCTGCTGATATC	60
Db	1	ATACGACGACGCTTACCGGTAAACGCTCAGATCTTCTGTTGAGCTTACCTGCTGATATC	60
Qy	61	ATTGCTGCTTACGTTCTTAAACAAGTTGTTCTGTTACTGACCTTCTGACCTTATCTCT	120
Db	61	GTGCGCGCTAATGTTTMSNAACAYGTTGTTCCGTTACGATGATTCGCGGTTATATMSN	120
Qy	121	GATGTTCAATCTGACCTTCTGGAACATCTGCTCTGCTCGTTGCTGTTACGTTAG	180
Db	121	GAATGTTCAATCGCATTTMSNGNACMSNGCCGCMSTGTTGCTGTTAAAGTTGATG	180
Qy	241	AAGCAGAAAGCTGCTGTTCTGTTGCTGAAGTCTGTTCAAGATCATATCGTTTGTGTTG	240
Db	181	AACCARAARCCGCGCTTMSNGTMMGNABRWSNGTNCARGAYGATATGTTGTYTIN	240
Qy	241	GAGTGTGCTGTTCTTTCAAGTCTCAAGCTCACTTACTATCATCTATATACT	300
Db	241	GATGTGTGCGGMSNTTAAARMSNTYNAARMENCAYYTNACNACNCAYCAVMSNATACN	300
Qy	301	CCAGAGAGATATGAGAGAAGATGGAGTCTTCTGTTGATTAACCTATGTTGCTCTGCT	360
Db	301	CCGAGARATATYMGNGARPAARATGGGAYTINCCGTTNGATYTAACATGTTGCMCCGCGN	360
Qy	361	TACGTTGAGGCTGTTCTGCTCTCGCTACGTAAGAGATGGATCTCGGTCAAGCTCGTAAGCT	420
Db	361	TAYGCGNARGCNGNMNGNMYTNGCNAARGARATGGGNTYNGCARMGMMGAAGCN	420
Qy	421	AACCGTCCAAAAAGAACGCTAAGCT 446	
Db	421	AAATGNCNNAARARAAARMAAAGT 446	

RESULT 9
AAD52860
ID AAD52860 standard; DNA; 429 BP.

AC AAD52860;
XX
DT 14-MAY-2003 (first entry)
XX
DE Agrobacterium tumefaciens ros repressor DNA
XX
KW ROS repressor protein; gene expression; ds.
XX
OS Agrobacterium tumefaciens.
XX
PN W0200295021-A2.
XX
PD 28-NOV-2002.

XX 23-MAY-2002; 2002WO-CA000740
PF
VV

PR 23-MAY-2001; 2001US-0292973P

PA (MIAC) CANADA DEPT AGRIC & AGRI-FOOD CANADA.
VV

PI Hannoufa A, Hegedus D, Bate N;

DR WPI; 2003-148467/14.

PT New nucleic acid molecule encoding a ROS repressor, useful for
PT controlling gene expression in plants, comprises a regulatory region
PT operatively linked to a gene of interest and one or more ROS operator
PT sequence.

PS Example 1; Page 69; 84pp; English

CC The present invention relates to a novel nucleic acid molecule encoding a
CC ROS repressor protein optimised for plant codon usage and exhibiting ROS
CC operator binding activity and/or ROS repressor activity. The nucleic acid
CC molecule comprises a regulatory region operatively linked to a gene of
CC interest and one or more ROS operator sequence capable of controlling the
CC activity of the regulatory region that is functional in plants. They are
CC useful in controlling gene expression in plants using a repressor protein
CC and corresponding operator sequences. The present sequence is
CC *Agrobacterium tumefaciens* ros repressor DNA. NOTE: This sequence is said
CC to encode the repressor protein shown as SEQ ID NO: 21 in page 76 of the
CC specification. However this does not appear to be the case

Sequence 429 BP; 94 A; 115 C; 126 G; 94 T; 0 U; 0 Other.

Query Match	63.7%	Score 291.6;	DB 8;	Length 429;
Best Local Similarity	80.3%	Pred NO. 1	8e-73;	

Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

OY	1	ATGACTGAGACTGCTTACGGTAACGCTCAGGATCTCTTGTGTGAGCTTACCTGCTGATATC	60
Db	1	ATGACGGAAATCTGCATACGGTAAACGCCAAGGATCTGTGGTGAACCTGAACGGCGGATATT	60
OY	61	GTGTGCTGTAACTGTTTCTTAACCAAGTGTTCCTGTTACTGACCTTCGGACTTATCTCT	120
Db	61	GTGGCTGCTATGTTAAGCAACCACTGCTGTCCGGTAACCTGACCTTCCGGCTTATTTGG	120
OY	121	GATGTTCACTACGCACTTTCTGGAACATCTGCTCTGCTTCTGTTGCTTTAACTGTAG	180
Db	121	GATGTTCAATACGGCACTACGCGGAACATCTGCAACCGGATCGGTGGCGGCTCAATGTTGA	180
OY	181	AAGCAGAAAGCTGCTGTTTCTGTTGTAAGTCTGTTCAAGATGATCAATATCGTTTGTG	240
Db	181	AAGCAGAAAGCTGCTGCTGTGCGGTTGCGAAAGTGGTTACAGAACATCATATCGTCTTTTG	240
OY	241	GAGTGTGCTGTTCTTTTCAAGTCTCTCAAGCTCACCTTATCACTCATCACTATAGACT	300
Db	241	GAATGTGTGCTCGTTCAAGTCTCAAAAGCCACTGACACGATATACAGCATAGACG	300
OY	301	CCAGAGAGTATAGAGAGAAGTGGATCTTCTGTGTGATTAACCTATATGTTGCTCTGTCT	360
Db	301	CCGGAAGATATCCGGAATAATGGGATCTGCCCGTGGATATCCGATGGTGTCTCCGCC	360
OY	361	TACGCTGAGGCTCGTTCTGCTCGCTAAAGAGATGGTCTTCGGTCAAGCTGTGAAGGCT	420
Db	361	TATGCGGAAGCCGTTCCGCGCTCCACCAAGGAATAAGGCTCTCGGTCAAGCGCGCAAGGCG	420
OY	421	AAACGT 426	
Db	421	AAACGT 426	

RESULT 10
AAL56363
ID AAL56363 standard; DNA; 429 BP
XX

AC AAL56363;
 XX
 XX 22-APR-2004 (first entry)
 XX
 XX A tumefaciens ROS gene.
 DE Gene expression system; plant; ROS; vector; metabolic engineering; gene;
 KM ds.
 OS Agrobacterium tumefaciens.
 XX
 XX W02003100063-A1.
 PN
 XX
 XX 04-DEC-2003.
 PD
 XX
 XX 21-NOV-2002; 2002MO-CA001807.
 PF
 XX
 XX 23-MAY-2002; 2002MO-CA000740.
 PR
 XX (MIAC) CANADA MIN AGRIC & AGRI-FOOD.
 PA
 XX Hannoufa A, Hegedus D, Bate N;
 PI WPI; 2004-035150/03.
 PS
 XX New nucleic acids encoding a ROS repressor optimized for plant codon
 PT usage and exhibits ROS operator binding activity, ROS repressor activity
 PT or both, useful for regulating gene expression in plants.
 XX
 XX Disclosure; Page 90-91; Opp; English.
 PS
 XX The present invention relates to a nucleic acid construct comprising a
 CC regulatory region operatively linked to a gene of interest and one or
 CC more ROS operator sequence capable of controlling the activity of the
 CC regulatory region which is functional in plants, encodes a ROS repressor
 CC optimized for plant codon usage and exhibits ROS operator binding
 CC activity, ROS repressor activity or both. The nucleic acid molecule or
 CC its derivative is useful for the regulation of gene expression in plants.
 CC The gene expression can be used in metabolic engineering to produce
 CC plants that accumulate large amounts of certain intermediate compounds.
 CC The present sequence is a polynucleotide used in constructs of the
 CC invention
 CC
 XX
 XX Sequence 429 BP; 94 A; 115 C; 126 G; 94 T; 0 U; 0 Other;
 SQ
 Query Match 63.7%; Score 291.6; DB 12; Length 429;
 Best Local Similarity 80.3%; Pred. No. 1.8e-73;
 Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
 QY 1 ATGACTGAGACTGCTTACGCTAAGCATCTCTCTGTTGAGCTTACTGATATC 60
 DB 1 ATGACGGAAGTGCATCGATACGCTAAGCATCTCTCTGTTGAGCATGACGCGGATAT 60
 QY 61 GTTCTGCTTACGTTTCTTACCAAGCTGTTCTGTTACTGAGCTTCTGACTATCTCT 120
 DB 61 GTTGCTGCTATGTTAGCAACCAAGTGTCTGTTACTGAGCTTCTGCGCTTATTTG 120
 QY 121 GATGTCATCTGACCTTCTGGAACATCTGCTGCTTCTGTTGCTGTTAACTGAG 180
 DB 121 GATGTCATCTGACCTTCTGGAACATCTGCTGCTTCTGTTGCTGTTAACTGAG 180
 QY 181 AAGCAGAAGCTGCTGTTCTGTTCTGTTAAGTCTGTTGAGATGATATGTTGTTG 240
 DB 181 AAGCAGAAGCTGCTGTTCTGTTCTGTTAAGTCTGTTGAGATGATATGTTGTTG 240
 QY 241 GAGTGTGCTGTTCTTTCAGATCTCTCAAGGCTCACTTACTACTCTATAGACT 300
 DB 241 GAGTGTGCTGCTGTTCTTTCAGATCTCTCAAGGCTCACTTACTACTCTATAGACT 300
 QY 301 CCAGAGAGATATAGAGAGATGAGATCTTCTGTTGATTAAGCTATAGGTTGCTCTGCT 360
 DB 301 CCAGAGAGATATCGGAAATGAGATCTGCTGTTGATTAAGCTATAGGTTGCTCTGCT 360

QY 361 TAGCTGAGGCTGCTTCTGCTCTGCTTAAGAGATGGTCTCGGTACGCTCTAAGCT 420
 DB 361 TAGCGGAGAGCCGCTTCTGCGGCTCGCCAGAAATGGTCTCGGTACAGCGCGCAAGCGC 420
 QY 421 AACCGT 426
 DB 421 AACCGT 426
 QY 421 AACCGT 426
 DB 421 AACCGT 426
 RESULT 11
 ADR22405
 ID ADR22405 standard; DNA; 429 BP.
 AC ADR22405;
 XX
 XX 07-OCT-2004 (first entry)
 DT
 XX
 XX Agrobacterium tumefaciens wild-type Ros selectable marker DNA.
 DE
 XX repressor-mediated plant selection; transgenic; antibiotic resistance;
 KM wild-type; Ros selectable marker; ds; gene.
 XX
 XX Agrobacterium tumefaciens.
 OS
 XX
 XX Key Location/Qualifiers
 FH CDS 1..429
 FT /tag= a
 FT /product= "Agrobacterium tumefaciens wild-type Ros
 FT selectable marker protein"
 XX
 XX CA2442521-A1.
 PN
 XX
 XX 03-APR-2004.
 PD
 XX
 XX 03-OCT-2003; 2003CA-02442521.
 PF
 XX
 XX 03-OCT-2002; 2002US-0416369P.
 PR
 XX (MIAC) CANADA MIN AGRICULTURE.
 PA
 XX Hannoufa A, Bate N, Hannoufa A, Lydiate D;
 PI Hegedus D, Bate N, Hannoufa A, Lydiate D;
 PS
 XX WPI; 2004-341154/32.
 DR P-PSDB; ADR22407.
 XX
 XX Receptor-mediated plant selection strategies to identify transgenic
 PT plants comprising using a selectable marker system for plant
 PT transformation that is benign to the plant and confers no advantage to
 PT other organisms after gene transfer.
 XX
 XX Example 2; SEQ ID NO 19; 125bp; English.
 PS
 XX The invention relates to novel repressor-mediated plant selection
 CC strategies to identify and select plants, cells, tissue or entire plants
 CC which comprise a coding region of interest. The methods of the invention
 CC may be used for selecting transgenic plants, cells, tissue or entire
 CC plants which comprise a coding region of interest. The methods are not
 CC based on antibiotic resistance, are simple to carry out and provide a
 CC selectable marker system for plant transformation that is benign to the
 CC transformed plant and confers no advantage to other organisms in the
 CC event of gene transfer. The methods involve stringent selection of
 CC transformed cells and use an inexpensive and effective selection agent
 CC that is non-toxic to plant cells. The current sequence is that of the
 CC Agrobacterium tumefaciens wild-type Ros selectable marker DNA of the
 CC invention.
 CC
 XX
 XX Sequence 429 BP; 94 A; 115 C; 126 G; 94 T; 0 U; 0 Other;
 SQ
 Query Match 63.7%; Score 291.6; DB 12; Length 429;
 Best Local Similarity 80.3%; Pred. No. 1.8e-73;
 Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
 QY 1 ATGACTGAGACTGCTTACGCTAAGCATCTCTCTGTTGAGCTTACTGATATC 60

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Db      1 ATAGCGAAACTGCATACGGTTAACGCCAAGATCTGCTGATCGAAGTCAAGCGCGGATATT 60
Qy      61 GTTGCTGCTTACGTTTCTTAACACGTTGTTCTGTGTAATGAGCTTCTGAGATTATCTCT 120
Db      61 GTGGCTGCTATGTATGACCAACAGTGTCTCCGGTAACTAGAGCTTCCGGCTTATTTG 120
Qy      121 GATGTCATCTGACCTTCTGGAACATCTGCTTCTGCTTCTGTGTGTTAAGTTGAG 180
Db      121 GATGTCATCTGACCTTCTGGAACATCTGCTTCTGCTTCTGTGTGTTAAGTTGAG 180
Qy      181 AACGAGAGCTGCTGTTTCTGTTCTGTAAGTCTGTGAGATGATCATATGTTGTTG 240
Db      181 AACGAGAGCTGCTGTTTCTGTTCTGTAAGTCTGTGAGATGATCATATGTTGTTG 240
Qy      241 GAGTGTGTTGTTCTTTCAAGTCTCTCAAGCTCACTTAATCTATCATCTATGACT 300
Db      241 GAGTGTGTTGTTCTTTCAAGTCTCTCAAGCTCACTTAATCTATCATCTATGACT 300
Qy      301 CCGAGAGAGTATGAGAGAGTGGATCTTCTGTTATTAACCTATGTTGCTCTGCT 360
Db      301 CCGAGAGAGTATGAGAGAGTGGATCTTCTGTTATTAACCTATGTTGCTCTGCT 360
Qy      361 TAGGCTAGAGCTGCTTCTGCTCTGCTAAGAGATGAGTCTGCTGAGCTGCTAAGGCT 420
Db      361 TAGGCTAGAGCTGCTTCTGCTCTGCTAAGAGATGAGTCTGCTGAGCTGCTAAGGCT 420
Qy      421 AACCGT 426
Db      421 AACCGT 426

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RESULT 12

AAV30458_0

WP Sequence split into 6 fragments LOCUS AAV30458 Accession Aav30458

Fragment Name

Begin

End

1 110000

AAV30458_1 100001 210000

AAV30458_2 200001 310000

AAV30458_3 300001 410000

AAV30458_4 400001 510000

AAV30458_5 500001 534720

AAV30458 standard; DNA; 534720 BP.

AAV30458;

14-OCT-1998 (first entry)

Rhizobium species plasmid pNGR234a.

Symbiosis; open reading frame; ORF; plasmid; vector; transportation;
degradation; metabolism; host range; nitrogen fixation; nodulation;
legume; plant; ds.

Rhizobium sp.

Location/Qualifiers

41796..418671

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/standard_name= "ORF K1"

/product= "oligopeptide permease"

/note= "homologous to the OprC gene"

418673..419680

/tag= b

/standard_name= "ORF K2"

/product= "oligopeptide permease"

/note= "homologous to the OprD gene"

419677..420738

/tag= c

/standard_name= "ORF K3"

/product= "oligopeptide permease"

/note= "homologous to the OprF gene"

420774..422159

/tag= d

/standard_name= "ORF K4"

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FT      /note= "homologous to the CapA gene"
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FT      /tag= e
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FT      /product= "aminotransferase-like protein"
FT      /note= "homologous to the BioA gene"
FT      424056..425594
FT      /tag= f
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FT      /product= "(semi) aldehyde dehydrogenase-like protein"
FT      /note= "homologous to the Tmp gene"
FT      428292..429623
FT      /tag= g
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FT      /note= "homologous to the Tmp gene"
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FT      /product= "protein of unknown function"
FT      /note= "homologous to the FixJ gene"
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FT      /product= "protein of unknown function"
FT      /note= "homologous to the FixJ gene"
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FT      /note= "homologous to the FdxN gene"
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FT      /tag= n
FT      /standard_name= "ORF K14"
FT      /gene= "nifB"
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FT      complement(436460..438130)
FT      /tag= o
FT      /standard_name= "ORF K15"
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FT      complement(438297..438590)
FT      /tag= p
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/gene= "fixA"
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/complement(442316..442636)
/tag= t
/standard_name= "ORF K20 /product= "protein of unknown function"
complement(443313..443879)
/tag= u
/standard_name= "ORF K21"
/product= "protein of unknown function"
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/note= "homologous to the NifQ gene"
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/standard_name= "ORF L2"
/product= "gamma-hexachlorocyclohexane-dechlorinase-like protein"
/note= "homologous to the LinA gene"
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/tag= z
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/product= "putative protein with degradative function"
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/gene= "nifD"
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FT /tag= ah
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FT /product= "protein similar to part of the Fe protein of nitrogenase"
FT /note= "homologous to the NifH gene"
FT CDS 461228..461545
FT /tag= ai
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FT /tag= aj
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Query Match 43.5%; Score 199.4; DB 2; Length 110000;
Best Local Similarity 67.4%; Pred. No. 4,5e-46;
Matches 281; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

Qy 1 ATGACTGAGCTGCTTAACGCTAAGCTCAGGATCTTGTGAGCTTACTGATATC 60
Db 16161 ATGACGAAACCAACGCTCGGTGAGCAACGATTTGGCAGACTGACGCGAATC 16220
Qy 61 GTTGCTGCTTACGTTCTTAACCAAGTTGCTCTTACTGAGCTTCTGACTTATCTC 120
Db 16221 GTAGCGCGCTATGTACAGACCCAGTGTTCCGGGTGCGAGCTTCGACGCTTACGCT 16280
Qy 121 GATGTTGATACCTGACCTTCTGGAACATGCTGCTGCTTCTTGTGTTAAGTTGAG 180
Db 16281 GACGTTCAATTCACGCTCAACATGCACTGCTCCGCGCGGTGATGCTCCCATTTGAG 16340
Qy 181 AAGCAGAGCTGCTGTTCTGTTGTAAGTCTGTCAGGATGATATATGTTTGTG 240
Db 16341 AAGCCGAGCAGCAGGCTGATCCGAGTCTGTGCGAGCATGATACCTGCTC 16400
Qy 241 GAGTGTGTGTTCTTTCAGTCTCAAGCGTCAACCTTACTGATCATCTATGACT 300
Db 16401 GAATGGGGCGGCGCTTCAAGTGTGTAAGCGGCACTTGATGATGCCACCAATCTGTG 16460
Qy 301 CCAGAGGATATGAGAGAACTGGGATCTTCTGTTGATTAACCTATGCTTCTCTGCT 360
Db 16461 CCGAAGATTATGCGCAAAAGTGGGACCTACCGCGAGATACCGGATGTGCGCCGCT 16520
Qy 361 TACGCTGAGGCTGTTCTGCTGCTGCTGCTAAGAGATGGGTCTCGATCAGCTGTAG 417
Db 16521 TATGCGAAGCCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16577

RESULT 13
AAV30459 0
WP Sequence split into 6 fragments LOCUS AAV30459 Accession AAV30459
WP Fragment Name Begin End
WP AAV30459_0 1 110000
WP AAV30459_1 100001 210000
WP AAV30459_2 200001 310000
WP AAV30459_3 300001 410000
WP AAV30459_4 400001 510000
WP AAV30459_5 500001 536165
ID AAV30459 standard; DNA; 536165 BP.
XX
XX AAV30459;
AC
XX
XX 06-JUL-1999 (first entry)
DT
XX
XX Rhizobium species symbiotic plasmid pNGR234.
DE
XX
XX Symbolic; open reading frame; ORF; plasmid; vector; transportation;
KW degradation; metabolism; host range; nitrogen fixation; nodulation;
KW legume; plant; ds.
XX
XX Rhizobium sp.
OS
XX


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Db      19841 CCTGATGGCTAAAGTACGGCCCTCAGCGCCGCAATATCGAGAGAAATGGGGTCTCCCGGC 19782
Qy      336  TGATTACCTTATGTTGCTCTGCTTACGCTGAGGCTCGTTCTGCTCTCGCTAAGAGAT 395
Db      19781 TGATTACCCCATGGTTGCTTCAAGCTATGCTCAAAAAGCGTTCCGAGCTTGGCGCGCTTT 19722
Qy      396  GGGTCTCGGTCAAGCGCTGTAAGG 419
Db      19721 GGGTCTGGGAAAGAAACGGAAGGC 19698
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Search completed: May 19, 2006, 22:40:46
Job time : 488 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2006, 01:14:38 ; Search time 3647 Seconds
(without alignments)
7022.499 Million cell updates/sec

Title: US-10-719-996A-2
Perfect score: 458
Sequence: 1 atgcactgcagactcgtcgcg.....cgttaagcttcgagctcgcg 458

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	24.9	401	11	AZ577265 07e12 Sho
2	95.6	20.9	257	11	AZ577928 1e11 Sho
3	65.2	14.2	782	11	BH202231 Sml-61C12
4	64	14.0	711	3	BMS588321 170006873
5	63	13.8	581	5	CF569196 EST057 Su
6	63	13.8	774	14	CR237539 Reverse 8
7	63	13.7	723	11	BH182027 020_K19-
8	62.6	13.7	723	11	BH182027 020_K19-
9	62.6	13.6	1933	6	AY325173 end of
10	62.4	13.5	475	11	BH209707 Sml-41P23
11	62	13.4	1429	10	DT996364 CNB184-A0
12	61.6	13.4	747	4	CB521826 UI-M-GH0-
13	61	13.3	482	11	BH184140 024_U22-
14	60.8	13.3	482	14	AL621093 T7 end of
15	60.8	13.3	639	11	AZ650033 IM0520C01
16	60.6	13.2	780	5	CF726920 UI-M-HB0-
17	60.6	13.2	818	11	BZ229437 CH230-401
18	60.4	13.2	711	11	BZ098560 CH230-235
19	60.4	13.2	711	11	BZ098560 CH230-235

20	60	13.1	676	8	CO041542 UI-M-F00-
21	59.6	13.0	479	2	Bj370460 Bj370460
22	59.4	13.0	410	11	BH211305 Sml-50G22
23	59.4	13.0	611	2	BM247568 K0803H04-
24	59.4	13.0	675	4	BY706450 BY706450
25	59.4	13.0	836	2	B1525376 602924305
26	59.4	13.0	917	4	CB181190 AGENCOURT
27	59.2	12.9	548	11	BH200391 Sml-39D16
28	58.8	12.8	936	10	DM609105 CGX199-A0
29	58.6	12.8	568	14	DE214279 Trifolium
30	58.6	12.8	906	14	DE214279 Trifolium
31	58.4	12.8	477	4	CA743784 wrlis.pk0
32	58.4	12.8	618	14	DE235981 Trifolium
33	58.2	12.7	704	3	BM478868 BM478868
34	58.2	12.7	710	8	CO543707 LYEST1134
35	58.2	12.7	732	11	BZ284533 CH230-385
36	58	12.7	695	2	Bj439038 Bj439038
37	58	12.7	695	2	Bj439038 Bj439038
38	58	12.7	970	14	CNS03H6V Z90761 F. rubripes
39	57.8	12.6	567	14	FR0006951 DM586149 PMAM-aa2
40	57.8	12.6	682	10	DM586149 PMAM-aa2
41	57.8	12.6	785	5	CK183608 EST772923
42	57.8	12.6	790	13	CZ280852 CP13901.r
43	57.8	12.6	819	13	CZ285019 CP38H09.r
44	57.8	12.6	854	4	BX078177 BX078177
45	57.6	12.6	487	11	BH200321 Sml-50G20

ALIGNMENTS

RESULT 1
AZ577265 401 bp DNA linear GSS 08-DEC-2000
LOCUS 07e12 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium
DEFINITION sp. NGR234 genomic clone 07e12, genomic survey sequence.

ACCESSION AZ577265.1 GI:11603506
VERSION GSS.
KEYWORDS Rhizobium sp. NGR234
SOURCE Rhizobium sp. NGR234
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium.

REFERENCE 1 (bases 1 to 401)
AUTHORS Viprey,V., Rosenthal,A., Broughton,W.J. and Perret,X.
TITLE Genetic snapshots of the Rhizobium species NGR234 genome
JOURNAL Genome Biol. 1 (6), RESEARCH0014 (2000)
PUBMED 11178268

COMMENT Contact: Virginie Viprey
Laboratoire de Biologie Moléculaire des Plantes Supérieures
Université de Genève
1 Chemin de l'Imperatrice, Chambesey/Genève 1292, Switzerland
Tel: +44(0)1603450000
Fax: +44(0)1603450045
Email: virginie.viprey@bbsrc.ac.uk
Class: shotgun.
Location/Qualifiers
1. 401
/organism="Rhizobium sp. NGR234"
/mol_type="genomic DNA"
/strain="ANU265"
/db_xref="taxon:394"
/clone="07e12"
/clone_lib="Shot-gun genomic library of Rhizobium strain ANU265"
/note="Vector: M13; derivative strain of NGR234 cured of pNGR234a"

FEATURES

source
1. 401
/organism="Rhizobium sp. NGR234"
/mol_type="genomic DNA"
/strain="ANU265"
/db_xref="taxon:394"
/clone="07e12"
/clone_lib="Shot-gun genomic library of Rhizobium strain ANU265"
/note="Vector: M13; derivative strain of NGR234 cured of pNGR234a"

ORIGIN

Query Match 24.9%; Score 114; DB 11; Length 401;
Best Local Similarity 65.8%; Pred. No. 2.4e-21;
Matches 196; Conservative 0; Mismatches 100; Indels 2; Gaps 2;

Qy 1 ATGACTGAGCTGCTTACGGTAAAGCTCAGAGATCTTGTGTAGCTTACTGCTGATATC 60
 |||||
 Db 101 ATGAGTGAAGATACGCTTCGGTGGAGCAAGAACTCCTGTTGAGCTGAGCGGGAATTC 160
 |||||
 Qy 61 GTTGCTGCTTACGTTTCTAAACACGTTGTCTGTACTAGAGCTTCTGACCTTAATCTT 120
 |||||
 Db 161 GTTGCCCGCTACGAGCAACACAGTGTTCCTGGTTCGAGGCTCCGACGCTGATATGCC 220
 |||||
 Qy 121 GAGTGTATCTGACCTTTCGGAACATCTGCTCTCTCTGTGTGTTAAGCTTGTAG 180
 |||||
 Db 221 GACCTTATTCGGGCTCAACATATACAGGCTCCGCGCGGTAGTCGCGGCTGAA 280
 |||||
 Qy 181 AAGCAGAGCCTGC-TGTTCTGTTCTGTAAGTCTGTTCAGAGATGATATCTGTTCTT 239
 |||||
 Db 281 AAGCGAAGCGCGGGGTTTCCTGCGAAGTGTGTCAGAGACAGACATCACTTCCCT 340
 |||||
 Qy 240 GGAATGCG-TGTTCTTTCAGTCTCTCAAGCTCACCTTACTACTCATCTAT 296
 |||||
 Db 341 CGAATCGCGGGGCTACCTTCMAATGCTGAAGCCCATTTGATGACCCACCAATCT 398
 |||||

RESULT 2
 A2577928 257 bp DNA linear GSS 08-DEC-2000
 LOCUS 16e11 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium
 DEFINITION sp. NGR234 genomic clone 16e11, genomic survey sequence.
 ACCESSION A2577928
 VERSION A2577928.1 GI:11604694
 KEYWORDS GSS.
 SOURCE Rhizobium sp. NGR234
 ORGANISM Rhizobium sp. NGR234
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 Rhizobiaceae; Rhizobium.

REFERENCE
 AUTHORS Vipey,V., Rosenthal,A., Broughton,W.J. and Perret,X.
 TITLE Genetic snapshots of the Rhizobium species NGR234 genome
 JOURNAL Genome Biol. 1 (6), RESEARCH0014 (2000)
 PUBMED 11178268
 COMMENT Contact: Virginie Vipey
 Laboratoire de Biologie Molculaire des Plantes Supérieures
 Université de Genève
 1 Chemin de l'Imperatrice, Chambesey/Geneva 1292, Switzerland
 Tel: +44(0)1603450000
 Fax: +44(0)1603450045
 Email: virginie.vipey@dbarc.ac.uk
 Class: shotgun;
 Location/Qualifiers

FEATURES
 source
 1..257
 /organism="Rhizobium sp. NGR234"
 /mol_type="genomic DNA"
 /strain="ANU265"
 /db_xref="taxon:394"
 /clone="16e11"
 /clone_lib="Shot-gun genomic library of Rhizobium strain
 ANU265"
 /note="Vector: M13; derivative strain of NGR234 cured of
 pNGR234a"

ORIGIN

Query Match 20.9%; Score 95.6; DB 11; Length 257;
 Best Local Similarity 67.3%; Pred. No. 4e-16;
 Matches 134; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
 Qy 29 AGAATCTTCTGTGAGCTTACTGATATCTGCTGCTTACTGTTCTTAACACAGCTTG 88
 |||||
 Db 59 ACGAATCTCTGTGAGCTGAGCGGGAATCTGTGCGCTACGAGCAACACAGCTGG 118
 |||||
 Qy 89 TTCTGTTACTGAGCTTCTGAGCTTATCTCGATGTTTATGATGACATTTCTGGAACAT 148
 |||||
 Db 119 TTCCGTTGCGGAGCTGCGAGCTGATGCGAGCTTCACTTCGCGCTCAACATACAA 178
 |||||
 Qy 149 CTGCTCTGCTTCTGTGTGCTGTAAAGCTTGAAGACAGAACCTGCTGTTTCTGTGTA 208
 |||||

Db 179 CGGCTCCCGCGCGGAGTGTGTCGCGGTGCAAAAGCCGCGGTTTCCGTTGCA 238
 |||||
 Qy 209 AGCTGTTCAAGATGATCA 227
 |||||
 Db 239 AATCGGTGAGAGACAACA 257
 |||||

RESULT 3
 BH202231/c 782 bp DNA linear GSS 15-NOV-2002
 LOCUS Sml-61C12.TR Sml Schistosoma mansoni genomic clone Sml-61C12,
 DEFINITION genomic survey sequence.
 ACCESSION BH202231
 VERSION BH202231.1 GI:16374489
 KEYWORDS GSS.
 SOURCE Schistosoma mansoni
 ORGANISM Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 782)
 Shetty,J., Simpson,A., Malek,J., Koo,H., Loverde,P.T. and
 El-Sayed,N.M.

REFERENCE
 AUTHORS Shetty,J., Simpson,A., Malek,J., Koo,H., Loverde,P.T. and
 El-Sayed,N.M.
 TITLE Use of end sequences from Schistosoma mansoni (Puerto Rico strain)
 JOURNAL Sml BAC library for gene discovery and map construction
 COMMENT Unpublished (2001)
 Other GSSs: Sml-61C12.TR
 Contact: Najib M. El-Sayed
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 0208
 Email: nelsayed@tigr.org

Clones are derived from the Schistosoma mansoni (Puerto Rico) Sml
 BAC library. For clone availability, please contact Dr. Najib
 El-Sayed at TIGR (nelsayed@tigr.org) or Dr. Phillip Loverde at
 State University of New York, Buffalo, New York, USA
 (loverde@buffalo.edu)
 Seq primer: M13 Rev
 Class: BAC ends.
 Location/Qualifiers

FEATURES
 source
 1..782
 /organism="Schistosoma mansoni"
 /mol_type="genomic DNA"
 /strain="Puerto Rico"
 /db_xref="taxon:6183"
 /clone="Sml-61C12"
 /clone_lib="Sml"
 /note="Vector: pBelobAC11; Site 1: Hin dIII; Constructed
 in the laboratory of Dr. Denis Le Paslier at the Fondation
 Jean Dausset, CEPH, Paris, France. Briefly, Schistosoma
 mansoni agarose embedded DNA was partially digested with
 Hin dIII. High molecular weight fragments were ligated in
 pBelobAC11 digested with Hin dIII. The average insert size
 is 100 kb. Total clone coverage: approx. 7.95 X the
 haploid genome. Further information can be found in Le
 Paslier et al. (2000) Construction and characterization of
 a Schistosoma mansoni bacterial artificial chromosome
 library. Genomics 65: 87-94."

ORIGIN

Query Match 14.2%; Score 65.2; DB 11; Length 782;
 Best Local Similarity 54.1%; Pred. No. 2.7e-07;
 Matches 133; Conservative 0; Mismatches 113; Indels 0; Gaps 0;
 Qy 5 CTGAGACTGCTTACGAGCTCAGAGCTTCTTGTGAGCTTACTGCTGATATCGTTG 64
 |||||
 Db 405 CTGCTGTGCTGCTGCTGATGATGCTATGCTGCTGCTGCTGATGATGATG 346
 |||||
 Qy 65 CTGCTTACGTTTCTAACCAAGTTTCTTCTTACTGAGCTTCTCGAGCTTATCTGATG 124
 |||||
 Db 345 ATGCTCGCGCTGCTTATGATGCTGCTGATATCTGATGCTGCTGCTGATGATC 286
 |||||

QY 125 TTCAATACGACCTTTTGTGGAACATCTGCTCCGCTTCTGTGCTGTTAACTGGAAGC 184
 DB 285 CTGCTGTTCCTAAATGCTGCTGTTGATGATCTGCTGCTGCTGCTGCTGCTG 226
 QY 185 AGAAGCTGCTGTTTCTGTTCTGTAAGTCTGTTGAGATGATCATCTGTTGAGAGT 244
 DB 225 ATGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 166
 QY 245 GTGGTG 250
 DB 165 AAGTTG 160

RESULT 4
 BM588321 711 bp mRNA linear EST 25-FEB-2002
 LOCUS 17000687322518 A.Gam.ad.cdna.blood1 Anopheles gambiae cDNA clone
 DEFINITION 19600449697628 5', mRNA sequence.
 ACCESSION BM588321 GI:18884182
 VERSION EST.
 KEYWORDS Anopheles gambiae (African malaria mosquito)
 SOURCE Anopheles gambiae
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Culicidae; Anophelinae; Anopheles.

REFERENCE
 AUTHORS Holt R.A., Lin J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,
 Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
 Celera Anopheles gambiae EST project
 JOURNAL Unpublished (2002)
 COMMENT Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 240453151
 Fax: 2404534580
 Email: HoltRA@celera.com
 Plate: NU01004AAR row: F column: 14
 Seq primer: M13 Reverse.

FEATURES
 source
 1..711
 Location/Qualifiers
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449697628"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_1lb="A.Gam.ad.cdna.blood1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
 hours after human blood feeding. cDNA inserts >500 bp
 cloned directionally into pSport 1. Not 1 site is 3'.
 Clones available through the Malaria Research and
 Reference Reagent Resource Center (www.malaria.mr4.org)"

ORIGIN
 Query Match 14.0%; Score 64; DB 3; Length 711;
 Best Local Similarity 48.4%; Pred. No. 5.7e-07;
 Matches 178; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 5 CTGAGACTGCTTACGCTACAGATCTTCTGTTGAGCTTACTGATATCGTTG 64
 DB 643 CTGCTGGGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 584
 QY 65 CTGCTTACGCTTCTTACCAAGCTGTTCTCTGTACTGAGCTTCTGAGACTATCTGTG 124
 DB 583 CATCTGCTGTGCTGCAATCTGCTGTTGTTGCTGCTGCTGCTGCTGCTGCTG 524
 QY 125 TTCAATACGACCTTTTGTGGAACATCTGCTCCGCTTCTGTGCTGTTAACTGGAAGC 184
 DB 523 TTGCTGTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 464

QY 185 AGAAGCTGCTGTTTCTGTTCTGTAAGTCTGTTGAGATGATCATATGTTGTTGAGT 244
 DB 463 CTGCTGTTCCTAAATGCTGCTGTTGATGATCTGCTGCTGCTGCTGCTGCTG 404
 QY 245 GTGGTGTTCTTCAAGTCTCTCAAGCTGACCTTACTGATCATCTATGACTCCAG 304
 DB 403 TTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 344
 QY 305 AGGACTATAGAGAGAGAGGAGATCTTCTGTTGATTAACCTATGTTGCTCCTTACG 364
 DB 343 CGGCTGTGCTGCTGCTGTTGTTGTTGCTGTTGCTGCTGCTGCTGCTGCTGCTG 284
 QY 365 CTGAGCT 372
 DB 283 CTGATGTT 276

RESULT 5
 CF569196/c 581 bp mRNA linear EST 08-SEP-2004
 LOCUS EST057 Subtracted, Clontech (cat. # K1804-1) Triticum aestivum cDNA
 DEFINITION Clone FDC57 5', mRNA sequence.
 ACCESSION CF569196
 VERSION CF569196.1 GI:51921536
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
 clade; Pooidae; Triticeae; Triticum.

REFERENCE
 AUTHORS Xiao, K., Bai, G.H. and Carver, B.F.
 Nylon Filter Arrays Reveal Differential Expression of Expressed
 Sequence Tags in Wheat Roots Under Aluminum Stresses
 J. Integr. Plant Biol. 47 (7), 839-848 (2005)
 CONTACT: Guohua Bai
 USDA/ARS and Department of Agronomy
 Kansas State University
 Manhattan, KS 66506, USA
 Email: gbai@bear.agron.ksu.edu
 Seq primer: M13 Forward
 High quality sequence stop: 581.

FEATURES
 source
 1..581
 Location/Qualifiers
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="OK91G106"
 /db_xref="taxon:4565"
 /clone="FDC57"
 /issue_type="root"
 /clone_1lb="Subtracted, Clontech (cat. # K1804-1)"
 /note="EST from wheat (Triticum aestivum, cv. OK91G106)
 root in response to aluminum stresses"

ORIGIN
 Query Match 13.8%; Score 63; DB 5; Length 581;
 Best Local Similarity 53.4%; Pred. No. 1e-06;
 Matches 132; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 6 TGAGATGCTTACGCTACAGATCTTCTGTTGAGCTTACTGATATCGTTG 65
 DB 324 TGTACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265
 QY 66 TGTACTGTTTCAACACAGCTGTTCTCTGTACTGAGCTTCTGAGACTATCTGATG 125
 DB 264 TGTACTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 205
 QY 126 TCATATGACCTTTCTGGAACATCTGCTCCTGCTTCTGTTGCTTTAACTGGAAGCA 185
 DB 204 TGTCTGTTGTTGTTGCTGTTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTG 145
 QY 186 GAAAGCTGCTGTTTCTGTTCTGTAAGTCTGTTGATGATCATATGTTTGGAGTG 245

ACCESSION BH182027 GI:16285700
VERSION
KEYWORDS GSS.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoida; Schistosomatidae; Schistosoma.
AUTHORS 1 (bases 1 to 723)
TITLE Le Paslier, M.C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams, D.L., Johnston, D., Loyer, P.T., and Le Paslier, D. Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
JOURNAL Genomics 65 (2), 87-94 (2000)
PUBMED 10783255
COMMENT Other_GSSs: 020_K_19-21
Contact: Pierce RJ
INSERM U 167
Institut Pasteur de Lille
1 rue du Professeur A. Calmette, 59019-Lille, France
Tel: (33) (0)3 20877783
Fax: (33) (0)3 20877888
Email: Raymond.Pierce@pasteur-lille.fr
CNS sequencing ID=DG0AA020AF10BP1
Plate: 020 row: K column: 19
Seq primer: M13 reverse primer
Clase: BAC ends
High quality sequence stop: 723.
Location/Qualifiers
1. 723
/organism="Schistosoma mansoni"
/mol_type="genomic DNA"
/strain="Puerto-Rican"
/db_xref="taxon:6183"
/clone="020K19"
/sex="mixed"
/dev_stage="cercariae"
/lab_host="Biomphalaria glabrata"
/clone_1lb="SmbAC1"
/note="Vector: pBeloBAC 11; Site: 1: Hind III; Partially Hind III digested and size-selected S. mansoni cercarial DNA was ligated into Hind III digested pBeloBAC 11 vector and used to transform E. coli DH10B. The complete library contains 23808 clones from 4 independent staling-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold."

ORIGIN
Query Match 13.7%; Score 62.6; DB 11; Length 723;
Best Local Similarity 53.0%; Pred. No. 1.4e-06;
Matches 131; Conservative 1; Mismatches 115; Indels 0; Gaps 0;

QY 6 TGAGACTGCTTACGCTACGCTCAGATCTTCTGTTGAGCTTACTGCTGATATCTGTC 65
DB 283 TGAATGATGCTGATGCTGCGCTGCTTATGATGATGATGATGCTGCTGCTATGCTGC 224
QY 66 TGGTTACGTTTCTAACACGTTGTTCTGTTACTGAGCTTCTGGAATTATCTGATGT 125
DB 223 TGTGATGATCCTACGCTGCTCTAATGCTGCTGTTGATGATCCTGCTGCTCTAATGCTGC 164
QY 126 TCATACCTGACCTTTGGAACATCTGCTGCTTCTGTTGCTGTTAACTTGAAGCA 185
DB 163 TGGCTGCTGCTGCTGCTGCTGCTGCTGATGATGATGATGATGATGATGATGA 104
QY 186 GAAGCTGCTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 245
DB 103 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGA 44
QY 246 TGGTGGT 252
DB 43 TGAATGAT 37

RESULT 9

CNS07NIN/c
LOCUS 723 bp DNA linear GSS 30-NOV-2001
DEFINITION T3 end of clone 020AF10 of library SmbAC1 from strain Puerto-Rican of Schistosoma mansoni, genomic survey sequence.
ACCESSION AL618977 GI:16032481
VERSION
KEYWORDS
SOURCE
ORGANISM Schistosoma mansoni
REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoida; Schistosomatidae; Schistosoma.
AUTHORS 1 (bases 1 to 723)
TITLE Le Paslier, M.C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams, D.L., Johnston, D., Loyer, P.T., and Le Paslier, D. Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
JOURNAL Genomics 65 (2), 87-94 (2000)
PUBMED 10783255
COMMENT Other_GSSs: 020_K_19-21
Contact: Pierce RJ
INSERM U 167
Institut Pasteur de Lille
1 rue du Professeur A. Calmette, 59019-Lille, France
Tel: (33) (0)3 20877783
Fax: (33) (0)3 20877888
Email: Raymond.Pierce@pasteur-lille.fr
CNS sequencing ID=DG0AA020AF10BP1
Plate: 020 row: K column: 19
Seq primer: M13 reverse primer
Clase: BAC ends
High quality sequence stop: 723.
Location/Qualifiers
1. 723
/organism="Schistosoma mansoni"
/mol_type="genomic DNA"
/strain="Puerto-Rican"
/db_xref="taxon:6183"
/clone="020AF10"
/clone_1lb="SmbAC1"
/note="end : T3"

ORIGIN
Query Match 13.7%; Score 62.6; DB 14; Length 723;
Best Local Similarity 53.0%; Pred. No. 1.4e-06;
Matches 131; Conservative 1; Mismatches 115; Indels 0; Gaps 0;

QY 6 TGAGACTGCTTACGCTACGCTCAGATCTTCTGTTGAGCTTACTGCTGATATCTGTC 65
DB 283 TGAATGATGCTGATGCTGCGCTGCTTATGATGATGATGATGCTGCTGCTATGCTGC 224
QY 66 TGGTTACGTTTCTAACACGTTGTTCTGTTACTGAGCTTCTGGAATTATCTGATGT 125
DB 223 TGTGATGATCCTACGCTGCTCTAATGCTGCTGTTGATGATCCTGCTGCTCTAATGCTGC 164
QY 126 TCATACCTGACCTTTGGAACATCTGCTGCTTCTGTTGCTGTTAACTTGAAGCA 185
DB 163 TGGCTGCTGCTGCTGCTGCTGCTGCTGATGATGATGATGATGATGATGATGA 104
QY 186 GAAGCTGCTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 245
DB 103 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGA 44
QY 246 TGGTGGT 252
DB 43 TGAATGAT 37

RESULT 10
AY325173/c
LOCUS 1933 bp mRNA linear HTC 26-JUL-2003
DEFINITION Rattus norvegicus Aa2-050 mRNA, complete cds.
ACCESSION AY325173
VERSION AY325173.1 GI:33086523
KEYWORDS HTC.
SOURCE Rattus norvegicus (Norway rat)

ORGANISM	<i>Rattus norvegicus</i> Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurongnathi; Muridae; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 1933)
AUTHORS	Xu, C.S., Li, M.Q., Li, Y.C., Yang, K.J., Yan, H.M., Chang, C.F., Zhao, L.F., Ma, H., Wang, L., Wang, S.F., Han, H.P., Wang, G.P., Chai, L.Q., Yan, J.Y., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
TITLE	Liver regeneration after PH
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1933)
AUTHORS	Xu, C.S., Li, M.Q., Li, Y.C., Yang, K.J., Yan, H.M., Chang, C.F., Zhao, L.F., Ma, H., Wang, L., Wang, S.F., Han, H.P., Wang, G.P., Chai, L.Q., Yan, J.Y., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
TITLE	Direct Submission
JOURNAL	Submitted (15-06-2003) Henan Bioengineering Key Lab, Henan Normal University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R. China

FEATURES	location/Qualifiers
source	1. 1933 /organism="Rattus norvegicus" /mol_type="mRNA" /db_xref="taxon:10116"
CDS	41. .1927

[illegible]

Query Match	13.6%	Score 62.4;	DB 6;	Length 1933;
Best Local Similarity	47.9%;	Pred. No. 2.1e-06;		
Matches 180; Conservative	0;	Mismatches 196;	Indels 0;	Gaps 0

[illegible]

Db	1454	TGTTGCTGTTGTTGCT	1439
RESULT 11			
LOCUS	BH209707/c		
DEFINITION	BH209707	475 bp	DNA
ACCESSION	Sml-41P23.TF	Sml Schistosoma mansoni genomic clone	Sml-41P23,
VERSION	BH209707	Genomic survey sequence.	
KEYWORDS	BH209707.1	GI:16388592	
SOURCE	GSS.		
ORGANISM	Schistosoma mansoni		
REFERENCE	Schistosoma mansoni		
AUTHORS	Eukaryotes: Metazoa: Platyhelminthes: Trematoda: Digenea: Strigoididae, Schistosomatidae, Schistosomatidae, Schistosoma.		
TITLE	1 (bases 1 to 475)		
COMMENT	Shetty,J., Simpson,A., Malek,J., Koo,H., Loverde,P.T. and El-Sayed,N.M.		
	Use of end sequences from Schistosoma mansoni (Puerto Rico strain)		
	Sml BAC library for gene discovery and map construction		
	Unpublished (2001)		
	Contact: Najib M. El-Sayed		

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: neilsayed@tigr.org
Clones are derived from the *Schistosoma mansoni* (Puerto Rico) Sml
C library. For clone availability, please contact Dr. Najib
El-Sayed at tigr (neilsayed@tigr.org) or Dr. Phillip Loveade at
State University of New York, Buffalo, New York, USA
(loveade@buffalo.edu)
Seq primer: M13 For
Class: BAC ends.

FEATURES	SOURCE	LOCATION/Qualifiers
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		/organism="Schistosoma mansoni"
		/mol_type="genomic DNA"
		/strain="Puerto Rico"
		/db_xref="taxon:6183"
		/clone="Sm1-41P23"
		/clone_lib="Sm1"
		/note="Vector: pBelobAC11; Site 1: Hin dIII; Constructed in the laboratory of Dr. Denis Le Paslier at the Fondation Jean Dausset, CDRH, Paris, France. Briefly, Schistosoma mansoni agarose embedded DNA was partially digested with Hin dIII. High molecular weight fragments were ligated in pBelobAC11 digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 7.95 x the haploid genome. Further information can be found in Le Paslier et al. (2000) Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library. Genomics 65: 87-94."

ORIGIN	Query Match	13.5%	Score 62;	DB 11;	Length 475;
	Best Local Similarity	53.3%	Pred. No. 1.9e-06;		
	Matches 131;	Conservative	0;	Mismatches 115;	Indels 0; Gaps 0;
QY	5	CTGAGACGCTTAAAGGTAAAGCTCAGAGATCTCTTTGTTGGACCTTACTGCTGATATCGTGG	64		
DB	434	CTGATGCTGCTGCTGCTGATATGATATGATGCTGCTGCTGCTGATATGATATGATATGCTGG	375		
QY	65	CTGCTTACGTTTTCACCAAGCTTTCTCTGTTTACGAGCTTCCTGGAATTATCTGTATG	124		
DB	374	CTGCTGCTGAAGCTGCTGCTGTTATGATATCTGCTGTTGCTGAAAGCTGCTGCTGATGATGCTG	315		
QY	125	TTCACTACTGCACCTTTCGGAACATCTGCTCTGCTCTCTGTTGCTGTTTAACGTTGGAAGC	184		
DB	314	CTGCTGCTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGATATGATGATGATG	255		
QY	185	AGAAAGCCTGCTGTTCTTCTTTCGTAAAGTCTGTTACAGATGATCATATCGTTTGTTTGGAGT	244		

[illegible]

Matches	118;	Conservative	0;	Mismatches	94;	Indels	0;	Gaps	0;
QY	5	CTGAGACTGCTTACGCGTAAACGCTCAGAGATCTTCTGTGTTAGACTTACGCTGATATCGTGG	64						
Db	464	CTTCTGCTGCTGCTGTGTTGTTGCTGTTGTTCTGCTGTTGTTGCTGTTGTTGTTGTTGTTGCTGCTG	523						
QY	65	CTGCTTACGTTTCTTAAACCAAGTGGTCTGCTGCTTACTGATGCTTCCGAGACTTATCTGTGATG	124						
Db	524	CTGCTGTGTTGTTGCTGCTGCTGCTGTTGTTGCTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTG	583						
QY	125	TTCATACTGCACTTTCGTGAACAATCTGCTCTGCTTCTGTGCTGTGTTGCTGTAAACGTTGAGAGC	184						
Db	584	CTGTGCTGCTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGTTGTTGTTGTTGTTG	643						
QY	185	AGAAAGCTGCTGTTTCTGTTCTGTGCTGTAAGTCTGTT	216						
Db	644	TTCGTTGGAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	675						
RESULT 13									
CB521826/c		747 bp	mRNA	linear	EST 09-JUN-2003				
LOCUS		UI-M-GH0-ceo-a-21-0-UI.r1 NIH BMAP_GH0	Mus musculus	CDNA clone					
DEFINITION		IMAGE:6842110 5', mRNA sequence.							
ACCESSION		CB521826							
VERSION		CB521826.1							
KEYWORDS		GI:29355181							
SOURCE		EST.							
ORGANISM		Mus musculus (house mouse)							
		Mus musculus							
		Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
		Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;							
		Sciurognathi; Muroidae; Muridae; Murinae; Mus.							
REFERENCE		NIH-MGC http://mgc.nci.nih.gov/ .							
AUTHORS		1 (bases 1 to 747)							
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)							
JOURNAL		Unpublished (1999)							
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgapds-remail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mouse1.html (BMAP) This clone was contributed by the Brain Molecular Anatomy Project							
FEATURES									
source									
		The following repetitive elements were found in this cDNA sequence: 289-410, >(CAA)n#Simple_repeat 406-531, >(CAG)n#Simple_repeat Seq primer: PYX-5.							
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		1..747							
		/organism="Mus musculus"							
		/mol_type="mRNA"							
		/strain="C57BL/6"							
		/db_xref="taxon:10090"							
		/clone="IMAGE:6842110"							
		/tissue_type="Whole brain"							
		/dev_stage="1, 5, and 15 days newborn"							
		/lab_host="DH10B (T1 phage resistant)"							
		/clone_id="NIH_BMAP_GH0"							
		/note="Organ: Brain; Vector: PYX-Asc; Site:1: EcoR I; Site:2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGCTGAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): Gene Discovery in the							

ORIGIN

Query Match 13.3%; Score 60.8; DB 14; Length 482;
Best Local Similarity 52.8%; Pred. No. 4.2e-06;
Matches 131; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

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QY      5 CTGAGACTGCTTAACGTAACGCTCAGATCTTCTTGTGAGCTTACTGCTGATATCGTTG 64
      |||||
Db      354 CTATGCTGATGCTGCTGCTGCTGCTGATGATGATGCTGCCGCTTATGATGATGATG 295
      |||||
QY      65 CTGCTTACGTTTCTTAACCAAGTGTTCCTGTTACTGAGCTTCCGACTTATCTGTGATG 124
      |||||
Db      294 ATCTGCTGCTGCTTAATGATGCTGCTGATGATCTGCTGCTTAATGCTGCTGTTGATG 235
      |||||
QY      125 TTCAATCTGCACTTCTTGAACATCTGCTCCTGCTTCTGTTGCTTTAACGTTGAGAAC 184
      |||||
Db      234 ATCTGCTGCTGCTTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGATGATGATG 175
      |||||
QY      185 AGAAGCTGCTGTTTCTGTTGTAAGTCTGTTGAGATGATCAATATGTTGTTGAGT 244
      |||||
Db      174 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 115
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QY      245 GTGATGAT 252
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Db      114 ATGATGAT 107
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Search completed: May 20, 2006, 03:18:35
Job time : 3660 secs

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Accession	Sequence	Position
Db	16401 GAATCGCGCGCGCCCTTCAAGTCGCTGAAGCCCACTTATGACCAACCAATCTGTGG	16460
Qy	301 CCAGAGAGTATAGAGAGATGGGATCTTCTGTGATTACCTATGGTTGCTCCTGCT	360
Db	16461 CCGGAAAGATTATCGCGAAAGGCGACCTACCCCGAGCATACCGATGGTCGCGCCGCT	16520
Qy	361 TACGCTGAGGCGCTGTTCTGTCCTCGGTAGAGATGGGCTGCGGTAGGGCTGTAG	417
Db	16571 TATGCGGAGGCCCGCTCGCGCTCGGCGCAAGAGATAGCGCTCGCGAGCGCCCGAG	16577

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RESULT 2
US-09-214-808-1/C
; Sequence 1, Application US/09214808A
; Patent No. 6475793
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andie
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe
; APPLICANT: Broughton, William John
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; Patent No. 6475793
; TITLE OF INVENTION: Plasmid
; FILE REFERENCE: CARP0068
; CURRENT APPLICATION NUMBER: US/09/214, 808A
; CURRENT FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: PCT/IB97/00950
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-214-808-1

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Query Match	20.6%	Score 94.4	DB 3	Length 536165
Best Local Similarity	54.7%	Pred. No. 9.4e-17		
Matches	210	Conservative	0	Mismatches 171; Indels 3; Gaps 1
Qy	39	TTTGAAGCTTACTGCTGATATATCGTTGCTGCTTACGTTTCTAACACAGTTGTTCTGTTAC	98	
Db	320081	TCCTTGAAGCTGACAAAGCCGGGTGTCTCGGCTTACTGAGCCGCAATATGTTCTCTGCGGC	320022	
Qy	99	TGAGCTTCCTGCACTTATCTCGATGTTTATCTGACATTTCTGGAACATCT---GCTCC	155	
Db	320021	CGATCTGGCCACTCTTATTCACAGACGTAATCTCTGCTATGACAGCACTCTCAAGGAGA	319632	
Qy	156	TGCTTCTGTGCTGTTTAAAGTTGAGAGAGAGAAAGCTGCTGTTTCTGTTGTAAGTGT	215	
Db	319961	CAAGGCTGAGAGAGGCTGCCGTGGAAACAGAGGCGCCGCGCTCCCATCAAGAAAGTCAAGT	319902	
Qy	216	TCAGATGATCATATTCGTTGTTTGGAGTGTGTGTTCTTTCAAGTCTCTCAAGCGTCA	275	
Db	319901	GACCCACAGCTTCATCATATATGCTCTGAGAGACGGTAAAAATTCGCTGAAAGCCACA	319842	
Qy	276	CCTTACTACTCATCATCTATGACTCCAGAGAGATATGAGAGAAAGGGATCTTCTGT	335	
Db	319841	CCTGATGCGTAAAGTACAGGCGCTCACGCCGACATATTCGAGAAAAATGGGCTCTCCCGGC	319782	
Qy	336	TGATTACCCCTATGTTGCTCTGTCTTACGCTGAGGCTGTTCTGTTCTGCTCAAGAGAT	395	
Db	319781	TGATTACCCCATGTTGTTGTTTCAAGCTATGCTCAAAAGCGTTCCGAGCTTCGCGCGCTTT	319722	
Qy	396	GGGCTCTCGCTCAGCGCTGTAAAGC	419	
Db	319721	GGGCTCGGAGAGAAACGACCGC	319698	

RESULT 3
US-09-639-207-13/c
; Sequence 13, Application US/09639207

```

Patent No. 6815575
GENERAL INFORMATION:
APPLICANT: Kazem-Befarjani, Parsa
APPLICANT: Benzer, Seymour
TITLE OF INVENTION: AN ANIMAL MODEL OF POLYGLUTAMINE
TITLE OF INVENTION: TOXICITY, METHODS OF USE, AND MODULATORS OF POLYGLUTAMINE
TITLE OF INVENTION: TOXICITY
FILE REFERENCE: 06618-686001
CURRENT APPLICATION NUMBER: US/09/639,207
CURRENT FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: US 60/148,934
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/148,923
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: US 60/177,047
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/205,720
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 486
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic DNA
US-09-639-207-13

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Query Match	Similarity	14.8%	Score 68	DB 3	Length 486
Best Local	Similarity	48.7%	Pred. No. 2.9e-10		
Matches	185	Conservative	0	Mismatches	195
		Indels	0	Gaps	0
QY	8	AGACGTCTTAACGGTAACGCTCAGACATCTTCTTGTTAGACTTACGTCGTATATCGTTGCTG	67		
Db	447	AGTCGTGTGCGCTGCTGCTGTTGTTGCTGCTGCTGTTGCGTTCGACGCTGCTGTTGTGCTG	388		
QY	68	CTTACGTTTCTTAACCAAGTGTGTTGCTGTACTGAGCTCTCGAATCTATCTGATGTTG	127		
Db	387	CTGCTGTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	328		
QY	128	ATACTGCACCTTTCGGAACAATCTGCTCTGCTCTTGTTGCTGTTTAAACGTTGAGAAGACA	187		
Db	327	CTGCTGCGGTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	268		
QY	188	AGCCTGCTGTTTCTGTTGCTGAAGTCTGTTCAGAGATGATCATGCTTTGTTTGAGATGTG	247		
Db	267	TTCGCTGCTGCTGTTGCTGTTGTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	208		
QY	248	GTCGTTCTCTTCAAGTCTCTCAAGGTCACCTTACTACTCATCTATGACTCAGAGAG	307		
Db	207	CTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	148		
QY	308	AGTATAGAGAGATGGAGATCTTCTGTGATTAACCTTAGAGTGTGCTCTGTTACGCTG	367		
Db	147	CTGCTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	88		
QY	368	AGGCTCGTTTCGCTCGCTCGCT	387		
Db	87	TTCGCTGCTGCTGTTGCTGCT	68		

RESULT 4
 US-08-728-123A-1/c
 : Sequence 1, Application US/08728323A
 : Patent No. 5948676
 : GENERAL INFORMATION:
 : APPLICANT: Chang, Yuan
 : APPLICANT: Bohenzky, Roy A.
 : APPLICANT: Russo, James J.
 : APPLICANT: Edelman, Isidore S.
 : APPLICANT: Moore, Patrick S.
 : TITLE OF INVENTION: Immediate Early Protein From Kaposi's
 : TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA

NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1
LENGTH: 3489
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-1

Query Match 14.0%; Score 64; DB 3; Length 3489;
Best Local Similarity 46.9%; Pred. No. 1.1e-08;
Matches 199; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 5 CTGAGCTGCTTACGAGTACGATCTTCTGTTAGCTTACCTGATATCGTTG 64
DB 2331 CTCTAATCCTGCTCCTGCTCTCTAATCCTGCTCCTGCTCCTGCTCCTGCTC 2272
QY 65 CTGCTTACGTTTCTTACCAAGTTTCTGTTATGAGCTTCCGGAAGTATCTGATG 124
DB 2271 CTCTGCTGCTCCTGTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2212
QY 125 TTCTATCTGCACTTTCTGAAACATCTGCTCCTGCTTCTGTTAGCTTACGTTAGAG 184
DB 2211 CTGCTGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2152
QY 185 AGAAGCTGCTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 244
DB 2151 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2092
QY 245 GTGCTGCTTCTTCAAGTCTCTCAAGGCTACCTTATCTGATCATCTATGATCTGAG 304
DB 2091 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2032
QY 305 AGAGATAGAGAGAGAGAGAGATCTTCTGTTGATTACCTATGTTGCTTCTGCTTACG 364
DB 2031 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1972
QY 365 CTGAGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
DB 1971 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1912
QY 425 GTCC 428
DB 1911 CTGC 1908

RESULT 7

US-09-894-273-1/c
Sequence 1, Application US/09894273
Patent No. 6756203
GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Bailestas, Mary E.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/894,273
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/109,422
PRIOR FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1
LENGTH: 3489
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-894-273-1

Query Match 14.0%; Score 64; DB 3; Length 3489;
Best Local Similarity 46.9%; Pred. No. 1.1e-08;
Matches 199; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 5 CTGAGCTGCTTACGAGTACGATCTTCTGTTAGCTTACCTGATATCGTTG 64

DB 2331 CTCTAATCCTGCTCCTGCTCTCTAATCCTGCTCCTGCTCCTGCTCCTGCTCCTGCTC 2272
QY 65 CTGCTTACGTTTCTTACCAAGTTTCTGTTATGAGCTTCCGGAAGTATCTGATG 124
DB 2271 CTCTGCTGCTCCTGTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2212
QY 125 TTCTATCTGCACTTTCTGAAACATCTGCTCCTGCTTCTGTTAGCTTACGTTAGAG 184
DB 2211 CTGCTGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2152
QY 185 AGAAGCTGCTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 244
DB 2151 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2092
QY 245 GTGCTGCTTCTTCAAGTCTCTCAAGGCTACCTTATCTGATCATCTATGATCTGAG 304
DB 2091 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2032
QY 305 AGAGATAGAGAGAGAGAGATCTTCTGTTGATTACCTATGTTGCTTCTGCTTACG 364
DB 2031 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1972
QY 365 CTGAGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
DB 1971 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1912
QY 425 GTCC 428
DB 1911 CTGC 1908

RESULT 8

US-08-770-379-20
Sequence 20, Application US/08770379
Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-20

Query Match
Best Local Similarity 46.9%; Score 64; DB 2; Length 32207;
Matches 199; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 5 CTGAGACTGCTTACGGTAACGCTCAGAGATCTTCTTGTGAGCTTACTGCTGATATGCTTG 64
DB 19666 CTCTAATCTCTGCTCCTGCTCTCTAATCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTC 19725

QY 65 CTGCTTACGTTTCTTAACCAAGTGTTCCTGTTACTGAGCTTCCGGAAGTATCTCTGATG 124
DB 19726 CTCTGCTGCTCTGTTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 19785

QY 125 TTCACTACGCACTTTTGAAACATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 184
DB 19786 CTGCTGCTGCTCACTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 19845

QY 185 AGAAGCTGCTGTTTCTGTTTCTGTAAGTCTGTTTCAAGATGATCATATGTTTGGAGT 244
DB 19846 CTGATCTGCTGCTATC 19905

QY 245 GTGCTGCTCTTCAAGTCTCTCAAGGCTACCTTACTCTCATCTATGACTCTGAG 304
DB 19906 CTGCTGCTGCTCACTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATC 19965

QY 305 AGAGATATAGAGAGAGAGGAGATCTCTGTTTGAATACCTATGTTGTTGCTTACG 364
DB 19966 CTGCTGCTGCTCACTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATC 20025

QY 365 CTGAGGCTGCTTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 424
DB 20026 CTGCTGCTGCTCACTCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATC 20085

QY 425 GTCC 428
DB 20086 CTGC 20089

RESULT 9
US-08-757-669A-20
Sequence 20, Application US/08757669A
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08757,669A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 45185-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-669A-20

Query Match
Best Local Similarity 46.9%; Score 64; DB 3; Length 32207;
Matches 199; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 5 CTGAGACTGCTTACGGTAACGCTCAGAGATCTTCTTGTGAGCTTACTGCTGATATGCTTG 64
DB 19666 CTCTAATCTCTGCTCCTGCTCTCTAATCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTC 19725

QY 65 CTGCTTACGTTTCTTAACCAAGTGTTCCTGTTACTGAGCTTCCGGAAGTATCTCTGATG 124
DB 19726 CTCTGCTGCTCTGTTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 19785

QY 125 TTCACTACGCACTTTTGAAACATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 184
DB 19786 CTGCTGCTGCTCACTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATC 19845

QY 185 AGAAGCTGCTGTTTCTGTTTCTGTAAGTCTGTTTCAAGATGATCATATGTTTGGAGT 244
DB 19846 CTGATCTGCTGCTATC 19905

QY 245 GTGCTGCTCTTCAAGTCTCTCAAGGCTACCTTACTCTCATCTATGACTCTGAG 304
DB 19906 CTGCTGCTGCTCACTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATC 19965

QY 305 AGAGATATAGAGAGAGGAGATCTTCTGTTTGAATACCTATGTTGTTGCTTACG 364
DB 19966 CTGCTGCTGCTCACTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATC 20025

QY 365 CTGAGGCTGCTTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 424
DB 20026 CTGCTGCTGCTCACTCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATC 20085

QY 425 GTCC 428
DB 20086 CTGC 20089

RESULT 10
US-09-230-371A-20
Sequence 20, Application US/09230371A
Patent No. 6348586
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 20
LENGTH: 32207
TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2006, 01:15:29 ; Search time 1050 Seconds
(without alignments)
5359.749 Million cell updates/sec

Title: US-10-719-996A-2

Perfect score: 458
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Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues
Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	458	100.0	458	9	US-10-719-996A-2
2	458	100.0	458	10	US-10-995-951A-2
3	458	100.0	458	8	US-10-678-490-1
4	458	100.0	472	15	US-11-067-425A-2
5	317	69.2	447	9	US-10-719-996A-3
6	317	69.2	447	10	US-10-995-951A-3
7	317	69.2	447	15	US-11-067-425A-3
8	291.6	63.7	429	9	US-10-678-490-19
9	291.6	63.7	429	10	US-10-719-996A-1
10	291.6	63.7	429	10	US-10-995-951A-1
11	199.4	40.5	536165	3	US-09-939-964-1
12	94.4	20.6	536165	3	US-09-939-964-1
13	68	14.8	486	7	US-10-465-217-13
14	64	14.0	3489	3	US-09-894-273-1
15	64	14.0	3489	3	US-10-294-804-1
16	64	14.0	3489	9	US-10-194-046-1
17	60.2	13.1	3660	11	US-10-932-182A-2664

C 18	59.8	13.1	936	11	US-10-932-182A-166977	Sequence 166977.
C 19	59.2	12.9	204893	11	US-10-330-773-325	Sequence 325, App
C 20	57.6	12.6	439	3	US-09-864-761-20174	Sequence 20174, A
C 21	57.4	12.5	3150	3	US-09-938-842A-243	Sequence 243, App
C 22	57.4	12.5	3150	3	US-09-938-842A-243	Sequence 243, App
C 23	57.4	12.5	3150	3	US-09-938-842A-243	Sequence 14743, A
C 24	57.2	12.5	6604	3	US-09-822-846-491	Sequence 491, App
C 25	57.2	12.5	6604	3	US-09-880-107-1748	Sequence 1748, App
C 26	55.2	12.1	3862	13	US-11-097-143-1973	Sequence 1973, App
C 27	55.2	12.1	9614	13	US-11-097-143-1972	Sequence 1972, App
C 28	54.2	11.8	599	16	US-11-136-527-1310	Sequence 1310, App
C 29	54.2	11.8	599	16	US-11-136-527-1310	Sequence 5406, App
C 30	54.2	11.8	2718	8	US-10-793-639-376	Sequence 376, App
C 31	54.2	11.8	3218	8	US-10-451-467A-63	Sequence 63, App
C 32	53.8	11.7	1037	7	US-10-373-667-3	Sequence 3, App
C 33	53.8	11.7	1159	7	US-10-373-667-1	Sequence 1, App
C 34	53.8	11.7	1471	7	US-10-373-667-2	Sequence 2, App
C 35	53.6	11.7	1236	6	US-10-077-584-3	Sequence 3, App
C 36	53	11.6	2742	11	US-10-932-182A-75676	Sequence 75676, A
C 37	52.8	11.5	1400	10	US-10-450-763-18999	Sequence 18999, A
C 38	52.6	11.5	5505	12	US-10-524-823-2	Sequence 2, App
C 39	52.6	11.5	30191	11	US-10-330-773-631	Sequence 631, App
C 40	51.8	11.3	573	7	US-10-029-386-25433	Sequence 25433, A
C 41	51.4	11.2	231	11	US-10-932-182A-174235	Sequence 174235, A
C 42	50.6	11.0	279	11	US-10-932-182A-174387	Sequence 174387, A
C 43	50.4	11.0	186	11	US-10-932-182A-174145	Sequence 174145, A
C 44	50.4	11.0	2076	13	US-11-097-143-848	Sequence 848, App
C 45	50.4	11.0	2142	11	US-10-932-182A-5700	Sequence 5700, App

ALIGNMENTS

RESULT 1
US-10-719-996A-2
Sequence 2, Application US/10719996A
Publication No. US20040224412A1
GENERAL INFORMATION:
APPLICANT: Hannouti, Abdelali
APPLICANT: Hegedua, Dwayne
APPLICANT: Bate, Nicholas
TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Expression
FILE REFERENCE: 1096.021A
CURRENT APPLICATION NUMBER: US/10/719, 996A
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: PCT/CA02/00740
PRIOR FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/252,973
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 458
TYPE: DNA
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: synthetic ROS optimized for plant codon usage and encoding fusion
OTHER INFORMATION: of ROS and nuclear localization signal
US-10-719-996A-2

Query Match 100.0%; Score 458; DB 9; Length 458;
Best local similarity 100.0%; Pred. No. 1e-128;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATACGAGAGCTGCTTACGCTAGCGTCAAGATCTTGTGAGCTTACTGATATC	60
DB	1	ATACGAGAGCTGCTTACGCTAGCGTCAAGATCTTGTGAGCTTACTGATATC	60
QY	61	GTTCGCTTACGCTTCTAACCAAGTGTTCCTGTTACTAGAGCTTCGACTTATCTC	120
DB	61	GTTCGCTTACGCTTCTAACCAAGTGTTCCTGTTACTAGAGCTTCGACTTATCTC	120

QY 121 GATGTCATACGACTTTCGTAACATCTGCTCTCTCTCTGTTGCTGTAACGTTGAG 180
DB 121 GATGTCATACGACTTTCGTAACATCTGCTCTCTCTCTGTTGCTGTAACGTTGAG 180
QY 181 AAGCAGAAAGCTGCTGTTTCTGTTGTAAGTCTGTTCAAGATGATCATATGCTTTGTTG 240
DB 181 AAGCAGAAAGCTGCTGTTTCTGTTGTAAGTCTGTTCAAGATGATCATATGCTTTGTTG 240
QY 241 GAGTGTGAGTGTCTTCAAGTCTCTCAAGGCTGACCTTACTCATCATCTCAATGACT 300
DB 241 GAGTGTGAGTGTCTTCAAGTCTCTCAAGGCTGACCTTACTCATCATCTCAATGACT 300
QY 301 CCAGAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 360
DB 301 CCAGAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 360
QY 361 TAGCTGAGGCTGCTTCTGCTCTGCTCTGCTAAGAGATGCTGCTGCTGCTGCT 420
DB 361 TAGCTGAGGCTGCTTCTGCTCTGCTCTGCTAAGAGATGCTGCTGCTGCTGCT 420
QY 421 AACCGTCAAAAAAGAACGCTAAGGCTGAGAGCTGCG 458
DB 421 AACCGTCAAAAAAGAACGCTAAGGCTGAGAGCTGCG 458

RESULT 2

US-10-995-951A-2
Sequence 2, Application US/10995951A
Publication No. US20050245732A1
GENERAL INFORMATION:
APPLICANT: Hamoufa, A. et al.
TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Expression
FILE REFERENCE: 1096.021B
CURRENT APPLICATION NUMBER: US/10/995, 951A
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: PCT/CA02/01807
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: PCT/CA02/00740
PRIOR FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patent version 3.0
SEQ ID NO 2
LENGTH: 458
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic ROS optimized for plant codon usage and encoding fusion
US-10-995-951A-2

Query Match 100.0%; Score 458; DB 10; Length 458;

Best Local Similarity 100.0%; Pred. No. 1e-128; Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTAACGTAACGCTCAGGATCTTCTGTTGAGTTAGTATGATATC 60
DB 1 ATGACTGAGACTGCTTAACGTAACGCTCAGGATCTTCTGTTGAGTTAGTATGATATC 60
QY 61 GTTGCTGCTTAACGTTTCTGTTCAACAGTGTCTGTTACTGAGCTTCTGACTATCTCT 120
DB 61 GTTGCTGCTTAACGTTTCTGTTCAACAGTGTCTGTTACTGAGCTTCTGACTATCTCT 120
QY 121 GATGTCATACGACTTTCGTAACATCTGCTCTGCTCTGTTGCTGTTAAGTTGAG 180
DB 121 GATGTCATACGACTTTCGTAACATCTGCTCTGCTCTGTTGCTGTTAAGTTGAG 180
QY 181 AAGCAGAAAGCTGCTGTTTCTGTTGTAAGTCTGTTCAAGATGATCATATGCTTTGTTG 240
DB 181 AAGCAGAAAGCTGCTGTTTCTGTTGTAAGTCTGTTCAAGATGATCATATGCTTTGTTG 240
QY 241 GAGTGTGAGTGTCTTCAAGTCTCTCAAGGCTGACCTTACTCATCATCTCAATGACT 300
DB 241 GAGTGTGAGTGTCTTCAAGTCTCTCAAGGCTGACCTTACTCATCATCTCAATGACT 300

DB 241 GAGTGTGAGTGTCTTCAAGTCTCTCAAGGCTGACCTTACTCATCATCTCAATGACT 300
QY 301 CCAGAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 360
DB 301 CCAGAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 360
QY 361 TAGCTGAGGCTGCTTCTGCTCTGCTCTGCTAAGAGATGCTGCTGCTGCTGCT 420
DB 361 TAGCTGAGGCTGCTTCTGCTCTGCTCTGCTAAGAGATGCTGCTGCTGCTGCT 420
QY 421 AACCGTCAAAAAAGAACGCTAAGGCTGAGAGCTGCG 458
DB 421 AACCGTCAAAAAAGAACGCTAAGGCTGAGAGCTGCG 458

RESULT 3

US-10-678-490-1
Sequence 1, Application US/10678490
Publication No. US20040148649A1
GENERAL INFORMATION:
APPLICANT: Lydiate, Derek
APPLICANT: Hamoufa, Abdelali
APPLICANT: Bate, Nicholas
APPLICANT: Hegedus, Dwayne
TITLE OF INVENTION: Repressor Mediated Selection Strategies
FILE REFERENCE: 11089.0003.NPUS01
CURRENT APPLICATION NUMBER: US/10/678, 490
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/416,369
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patent version 3.1
SEQ ID NO 1
LENGTH: 472
TYPE: DNA
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: Synthetic Ros optimized for plant expression
US-10-678-490-1

Query Match 100.0%; Score 458; DB 8; Length 472;

Best Local Similarity 100.0%; Pred. No. 1e-128; Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTAACGTAACGCTCAGGATCTTCTGTTGAGTTAGTATGATATC 60
DB 15 ATGACTGAGACTGCTTAACGTAACGCTCAGGATCTTCTGTTGAGTTAGTATGATATC 74
QY 61 GTTGCTGCTTAACGTTTCTGTTCAACAGTGTCTGTTACTGAGCTTCTGACTATCTCT 120
DB 75 GTTGCTGCTTAACGTTTCTGTTCAACAGTGTCTGTTACTGAGCTTCTGACTATCTCT 134
QY 121 GATGTCATACGACTTTCGTAACATCTGCTCTGCTCTGTTGCTGTTAAGTTGAG 180
DB 135 GATGTCATACGACTTTCGTAACATCTGCTCTGCTCTGTTGCTGTTAAGTTGAG 194
QY 181 AAGCAGAAAGCTGCTGTTTCTGTTGTAAGTCTGTTCAAGATGATCATATGCTTTGTTG 240
DB 195 AAGCAGAAAGCTGCTGTTTCTGTTGTAAGTCTGTTCAAGATGATCATATGCTTTGTTG 254
QY 241 GAGTGTGAGTGTCTTCAAGTCTCTCAAGGCTGACCTTACTCATCATCTCAATGACT 300
DB 255 GAGTGTGAGTGTCTTCAAGTCTCTCAAGGCTGACCTTACTCATCATCTCAATGACT 314
QY 301 CCAGAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 360
DB 315 CCAGAGAGATATAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 374
QY 361 TAGCTGAGGCTGCTTCTGCTCTGCTCTGCTAAGAGATGCTGCTGCTGCTGCT 420
DB 375 TAGCTGAGGCTGCTTCTGCTCTGCTCTGCTAAGAGATGCTGCTGCTGCTGCT 434
QY 421 AACCGTCAAAAAAGAACGCTAAGGCTGAGAGCTGCG 458


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Db      435 AACGTCCTCAAAAAGAAAGCGTAAGCTCTGAGAGCTCC 472
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RESULT 4
US-11-067-425A-2
; Sequence 2, Application US/11067425A
; Publication No. US20050278609A1
; GENERAL INFORMATION:
; APPLICANT: Hannoufa, Abdelali
; APPLICANT: Lydiata, Derek J.
; APPLICANT: Gao, Ming-Jun
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING CHROMATIN REMODELLING FACTORS
; FILE REFERENCE: 270.78US11
; CURRENT APPLICATION NUMBER: US/11/067,425A
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US 10/516,753
; PRIOR FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: PCT/CA03/00822
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,088
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic ROS
US-11-067-425A-2

Query Match      100.0%; Score 458; DB 15; Length 472;
Best Local Similarity 100.0%; Pred. No. 1e-128;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGACTGAGACTGCTTACGGTAACGCTCAGAGATCTTGTGTGAGCTTACGCTGATATC 60
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Qy      61 GTTGCTGCTTACGCTTCTTAACCAAGTGTCTCTTACTAGAGCTTCCGAGACTTATCTCT 120
Db      75 GTTGCTGCTTACGCTTCTTAACCAAGTGTCTCTTACTAGAGCTTCCGAGACTTATCTCT 134
Qy      121 GATGTTCACTGCACTTCTTGGAACATCTGCTCTCTCTTGTGCTGTTAAAGTTGAG 180
Db      135 GATGTTCACTGCACTTCTTGGAACATCTGCTCTCTCTTGTGCTGTTAAAGTTGAG 194
Qy      181 AAGCAGAGAGCTGCTGTTCTGTTCCGTAAGTCTGTTGAGATGATCATTCGTTGTTG 240
Db      195 AAGCAGAGAGCTGCTGTTCTGTTCCGTAAGTCTGTTGAGATGATCATTCGTTGTTG 254
Qy      241 GAGTGTGAGTCTTCTTCAAGTCTCTCAAGGTCACCTTACTACTACTATGACT 300
Db      255 GAGTGTGAGTCTTCTTCAAGTCTCTCAAGGTCACCTTACTACTACTATGACT 314
Qy      301 CCAGAGAGATATGAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 360
Db      315 CCAGAGAGATATGAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 374
Qy      361 TAGGCTAGAGCTGTTCTGCTCTGCTCAAGAGATGAGTCTCGGTGAGCGCTCGTAAGGCT 420
Db      375 TAGGCTAGAGCTGTTCTGCTCTGCTCAAGAGATGAGTCTCGGTGAGCGCTCGTAAGGCT 434
Qy      421 AACCGTCCAAAAAGAAAGCGTAAGCTCTGAGAGCTCCG 458
Db      435 AACCGTCCAAAAAGAAAGCGTAAGCTCTGAGAGCTCCG 472

RESULT 5
US-10-719-996A-3
; Sequence 3, Application US/10719996A
; Publication No. US2004024412A1
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; GENERAL INFORMATION:
; APPLICANT: Hannoufa, Abdelali
; APPLICANT: Hegedua, Dwayne
; APPLICANT: Bate, Nicholas
; TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Express
; FILE REFERENCE: 1096.021A
; CURRENT APPLICATION NUMBER: US/10/719,996A
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: PCT/CA02/00740
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/292,973
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: ROS consensus sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: n is A or T or G or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: h is A or C or T/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: m is A or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: x is G or A
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: y is C/u or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: w is A or C/u
US-10-719-996A-3

Query Match      69.2%; Score 317; DB 9; Length 447;
Best Local Similarity 58.3%; Pred. No. 9.8e-86;
Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;

Qy      1 ATGACTGAGACTGCTTACGGTAACGCTCAGAGATCTTGTGTGAGCTTACGCTGATATC 60
Db      1 ATGACNGARACNGCNTATYAGNNAVGCNCAAGAYTNTGTNGATATNACNGNCAVATH 60
Qy      61 GTTGCTGCTTACGCTTCTTAACCAAGTGTCTCTTACTAGAGCTTCCGAGACTTATCTCT 120
Db      61 GTTGCTGCTTACGCTTCTTAACCAAGTGTCTCTTACTAGAGCTTCCGAGACTTATCTCT 120
Qy      121 GATGTTCACTGCACTTCTTGGAACATCTGCTCTCTGTTGATTAACGTTGAG 180
Db      121 GATGTTCACTGCACTTCTTGGAACATCTGCTCTCTGTTGATTAACGTTGAG 180
Qy      181 AAGCAGAGAGCTGCTGTTCTGTTCCGTAAGTCTGTTGAGATGATCATTCGTTGTTG 240
Db      181 AAGCAGAGAGCTGCTGTTCTGTTCCGTAAGTCTGTTGAGATGATCATTCGTTGTTG 240
Qy      241 GAGTGTGAGTCTTCTTCAAGTCTCTCAAGGTCACCTTACTACTACTATGACT 300
Db      241 GAGTGTGAGTCTTCTTCAAGTCTCTCAAGGTCACCTTACTACTACTATGACT 300
Qy      301 CCAGAGAGATATGAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 360
Db      301 CCAGAGAGATATGAGAGAAAGTGGATCTTCTGTTGATTAACCTATGTTGCTCTGCT 360
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Db 301 CCNAGARATAYMGNAGARATGGGAYTTCNCNGTNGATAYACCNATGTTNGCNCNGCN 360
Qy 361 TAGCTGAGGCTGCTCTGCTGCTTAAGGAGATGGGTCGGTCAAGCGTGTAAAGCT 420
Db 361 TAGCNGARCGCNGMNSMNGYTTNGCNAARARATGGGAYTTCNGCARMGNGMAARGCN 420
Qy 421 AACCGTCCAAAAGAAAGCGTAAAGT 446
Db 421 AAYMGNCCNAARARARARMAARGT 446

RESULT 6
US-10-995-951A-3
; Sequence 3, Application US/10995951A
; Publication No. US20050245732A1
; GENERAL INFORMATION:
; APPLICANT: Hannoufa, A. et al.
; TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Expression
; FILE REFERENCE: 1096.021B
; CURRENT FILING DATE: 2004-11-23
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/CA02/01807
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/CA02/00740
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Artificial
; OTHER INFORMATION: ROS consensus sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: n is A or T or G or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: h is a or c or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: m is a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: r is G or A
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: y is t/u or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: w is a or t/u
US-10-995-951A-3

Query Match 69.2%; Score 317; DB 10; Length 447;
Best Local Similarity 58.3%; Pred. No. 9.8e-86;
Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;

Qy 1 ATGACTGAGACTGCTTACGCTTAAGGATCTTCTTTGAGCTTACTGCTGATATC 60
Db 1 ATGACNGARCGCNGTATGAGNAAYGNCARGAYTYTNGTNGARITYTNAACNGCNGAYATH 60
Qy 61 GTTGCTGCTTAAGCTTTCAACAGCTTTCTGTTACTGAGCTTCCGGACTTATGCT 120
Db 61 GTNGCNGCTNATYGTWMAATCAIYGTNGTNCNGTNAACNGARITYTNAACNGAYATH 120
Qy 121 GATGTTCACTGACCTTTCTGGAACATCTGCTCTGCTTCTGTTGCTTAAGCTTGA 180

Db 121 GAYTNCAYACNCGNTYTNWSNGNACNWSNGCNCNGCWSNCTNGCNGTNAAYGTNGAR 180
Qy 181 AAGCAGAAGCTGCTCTTTCTGTTCTGTAAGTCTGTTCAAGATGATATATGCTTTTG 240
Db 181 AACCARAARCCNGCNGTNGMNSMNGYTTNGCNAARARATGGGAYTTCNGCARMGNGMAARGCN 240
Qy 241 GAGTGTGAGTCTTCAAGTCTCTCAAGCGTCACTTACTATCATCTATGACT 300
Db 241 GARTYGGNGCNGMNSNTTYAARMGNTYTNAAARMGNCAYTNAACNCAAYCAWMSNATGACN 300
Qy 301 CCNAGAGATAYAGAGAAAGTGGATCTTCTGTTGATTTACCTTATGTTGCTCTGCT 360
Db 301 CCNAGARATAYMGNAGARATGGGAYTTCNCNGTNGATAYACCNATGTTNGCNCNGCN 360
Qy 361 TAGCTGAGGCTGCTCTGCTGCTTAAGGAGATGGGTCGGTCAAGCGTGTAAAGCT 420
Db 361 TAGCNGARCGCNGMNSMNGYTTNGCNAARARATGGGAYTTCNGCARMGNGMAARGCN 420
Qy 421 AACCGTCCAAAAGAAAGCGTAAAGT 446
Db 421 AAYMGNCCNAARARARARMAARGT 446

RESULT 7
US-11-067-425A-3
; Sequence 3, Application US/11067425A
; Publication No. US20050278809A1
; GENERAL INFORMATION:
; APPLICANT: Hannoufa, Abdelali
; APPLICANT: Gao, Ming-Jun
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION USING CHROMATIN REMODELLING FACTORS
; FILE REFERENCE: 270.78US11
; CURRENT APPLICATION NUMBER: US/11/067,425A
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US 10/516,753
; PRIOR FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: PCT/CA03/00822
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,088
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Composite ROS Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(112)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (27)..(27)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36)..(36)

OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (93)..(93)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc_feature
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (99)..(99)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (105)..(105)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (108)..(108)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc_feature
LOCATION: (111)..(111)
OTHER INFORMATION: n is a, c, g, or t

FEATURE:
NAME/KEY: misc_feature
LOCATION: (114)..(114)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (120)..(120)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (126)..(126)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (132)..(132)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc_feature
LOCATION: (135)..(135)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (138)..(138)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (141)..(141)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (144)..(144)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (147)..(147)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (150)..(150)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (153)..(153)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (156)..(156)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (159)..(159)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (162)..(162)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (165)..(165)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (168)..(168)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (171)..(171)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (177)..(177)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:

NAME/KEY: misc feature
 LOCATION: (192)..(192)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (195)..(195)
 OTHER INFORMATION: n is a, c, g, or t

Query Match 69.2%; Score 317; DB 15; Length 447;
 Best Local Similarity 58.3%; Pred. No. 9.8e-86;
 Matches 260; Conservative 97; Mismatches 89; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACGCTTAACGCTTCTTCTTGTGAGCTTACTGCTGATATC 60
 DB 1 ATGACNBARACNCTATYAGNAAYGCNCARGAAYTNTNGTNGARYTNACNGCNGAYATH 60
 QY 61 GTTGCTGCTTACCTTCTTAAACGCTTGTCTTCTTCTGAGCTTCTGACTATCTCT 120
 DB 61 GTNCGNCTATYGTNMSNAAYCAVGTNGTNCNGTNAACNARYTNCCNGAYTNATHMSN 120
 QY 121 GATGTCATATGCACTTCTTGAACAATCTGCTCTCTCTTCTGCTGCTTAACTGAG 180
 DB 121 GAYTNCNAYACNCTNNTMSNGNAACNMSNCCNCCNMSNNGTNGCNGTAAATGTMGAR 180
 QY 181 AAGCAGAAAGCTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 181 AARCARBARCCNCGTNGTMSNGTNGAARMSNGTNGARAYCAVATHTGTGYTN 240
 QY 241 GAGTGTGCTGCTTCTTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCT 300
 DB 241 GARTGCGNCGNMSNTYTAARMSNTYTAARMSNTYTAARMSNTYTAARMSNTYTAAR 300
 QY 301 CCAGAGAGATATAGAGAAAGTGGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 301 CCNBARBARATYMGNGARARATGGAYTNTNCTNGATATATYCNATAGTNGCNCNGCN 360
 QY 361 TACGCTGAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 361 TAYCNGARCGCNMGNMSNGTNGAARARATGGAYTNGTNGCARMGNMNAARGCN 420
 QY 421 AACGTCGCAAAAAGAACGCTAAGT 446
 DB 421 AAYMNCNBAR 446

RESULT 8
 US-10-678-490-19
 Sequence 19, Application US/10678490
 Publication No. US20040148649A1
 GENERAL INFORMATION:
 APPLICANT: Lydiate, Derek
 APPLICANT: Hamoufa, Abdelali
 APPLICANT: Bate, Nicholas
 TITLE OF INVENTION: Repressor Mediated Selection Strategies
 FILE REFERENCE: 11089.0003.NPUS01
 CURRENT FILING DATE: 2003-10-03
 PRIOR APPLICATION NUMBER: US/10/678.490
 PRIOR FILING DATE: 2002-10-03
 NUMBER OF SEQ ID NOS: 61
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 19
 LENGTH: 429
 TYPE: DNA
 ORGANISM: Agrobacterium tumefaciens
 US-10-678-490-19

Query Match 63.7%; Score 291.6; DB 8; Length 429;
 Best Local Similarity 80.3%; Pred. No. 5.3e-78;
 Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACGCTTAACGCTTCTTCTTGTGAGCTTACTGCTGATATC 60

DB 1 ATGACGAAACGTCATACGCTTAACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 QY 61 GTTGCTGCTTACCTTCTTAAACGCTTGTCTGCTTACTGAGCTTCTGACTTATCTCT 120
 DB 61 GTTGCTGCTTATGTGACCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 QY 121 GATGTCATATGCTGCTTCTTGAACAATCTGCTCTGCTTCTGCTTCTGCTTAACTGAG 180
 DB 121 GATGTCATATGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 181 AAGCAGAAAGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 181 AAGCAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 241 GAGTGTGCTGCTTCTTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCT 300
 DB 241 GATGCTGCTGCTGCTTCTTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCTCTCAAGCT 300
 QY 301 CCAGAGAGATATAGAGAAAGTGGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 301 CCGGAAAGATATGCGCAAAAATGGATCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 361 TACGCTGAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 361 TATGCGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 421 AACCGT 426
 DB 421 AACCGT 426

RESULT 9
 US-10-719-996a-1
 Sequence 1, Application US/10719996A
 Publication No. US20040224412A1
 GENERAL INFORMATION:
 APPLICANT: Hamoufa, Abdelali
 APPLICANT: Hegedus, Dwayne
 APPLICANT: Bate, Nicholas
 TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Expression
 FILE REFERENCE: 1096.021A
 CURRENT FILING DATE: 2003-11-21
 PRIOR APPLICATION NUMBER: PCT/CA02/00740
 PRIOR FILING DATE: 2002-05-23
 PRIOR APPLICATION NUMBER: US 60/292,973
 PRIOR FILING DATE: 2001-05-23
 NUMBER OF SEQ ID NOS: 44
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 1
 LENGTH: 429
 TYPE: DNA
 ORGANISM: Agrobacterium tumefaciens
 US-10-719-996a-1

Query Match 63.7%; Score 291.6; DB 9; Length 429;
 Best Local Similarity 80.3%; Pred. No. 5.3e-78;
 Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACGCTTAACGCTTCTTCTTGTGAGCTTACTGCTGATATC 60
 DB 1 ATGACGAAACGTCATACGCTTAACGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 QY 61 GTTGCTGCTTACCTTCTTAAACGCTTGTCTTCTTCTGAGCTTCTGACTTATCTCT 120
 DB 61 GTTGCTGCTTATGTGACCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 QY 121 GATGTCATATGCTGCTTCTTGAACAATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 121 GATGTCATATGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180

QY 181 AAGCAGAGGCTGCTGTTTCTGTTCTGTTAAGTCTGTTGAGATGATCATATGTTTGG 240
DB 181 AAGCAGAGGCTGCTGTTGTTGCTGCTGCAAGTCTGTTCAAGATCATATGTTTGG 240
QY 241 GAGTGTGTTGTTCTTCTCAAGTCTCTCAAGCTCACTTACTACTACTATGTTTGG 300
DB 241 GAGTGTGTTGTTCTTCTCAAGTCTCTCAAGCTCACTTACTACTACTATGTTTGG 300
QY 301 CCAGAGAGTATAG 360
DB 301 CCAGAGAGATATGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 TAGCGTAGAGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 TAGCGTAGAGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 AACCGT 426
DB 421 AACCGT 426

RESULT 10
US-10-995-951A-1
; Sequence 1, Application US/10995951A
; Publication No. US20050245732A1
; GENERAL INFORMATION:
; APPLICANT: Hamoufa, A. et al.
; TITLE OF INVENTION: A Repressor-Mediated Regulation System for Control of Gene Expres
; TITLE OF INVENTION: Plasmids
; FILE REFERENCE: 1096 021B
; CURRENT APPLICATION NUMBER: US/10/995, 951A
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: PCT/CA02/01807
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/CA02/00740
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent version 3.0
; SEQ ID NO 1
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-995-951A-1

Query Match 63.7%; Score 291.6; DB 10; Length 429;
Best Local Similarity 80.3%; Pred. No. 5.3e-78;
Matches 342; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACCGTAAAGCTCAAGATCTTCTGTTGAGCTTACTGCTGATATC 60
DB 1 ATGACGAGAACTGATACGATACGATACGATACGATACGATACGATACGATACGATAT 60
QY 61 GTTGTGCTTACGTTTCTTAAACAGGTTGTTCTGTTAAGTCTTCTGAGCTTACTATCT 120
DB 61 GTTGTGCTTACGTTTCTTAAACAGGTTGTTCTGTTAAGTCTTCTGAGCTTACTATCT 120
QY 121 GATGTTCACTGATCTTCTGAAACATCTGCTCTGCTTCTGTTGCTGTTAAGTCTGAG 180
DB 121 GATGTTCACTGATCTTCTGAAACATCTGCTCTGCTTCTGTTGCTGTTAAGTCTGAG 180
QY 181 AAGCAGAGGCTGCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 240
DB 181 AAGCAGAGGCTGCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 240
QY 241 GAGTGTGTTGTTCTTCAAGTCTCTCAAGGCTCACTTACTACTACTACTATGACT 300
DB 241 GAGTGTGTTGTTCTTCAAGTCTCTCAAGGCTCACTTACTACTACTACTATGACT 300
QY 301 CCAGAGAGTATAG 360
DB 301 CCAGAGAGATATGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 TAGCGTAGAGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

DB 361 TAGCGTAGAGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 AACCGT 426
DB 421 AACCGT 426

RESULT 11
US-09-939-964-1
; Sequence 1, Application US/09939964
; Publication No. US20030054522A1
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andre
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe
; APPLICANT: Broughton, William John
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; TITLE OF INVENTION: Plasmid
; FILE REFERENCE: CAP0068
; CURRENT APPLICATION NUMBER: US/09/939, 964
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/214, 808
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-939-964-1

Query Match 43.5%; Score 199.4; DB 3; Length 536165;
Best Local Similarity 67.4%; Pred. No. 2.6e-48;
Matches 281; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 1 ATGACTGAGACTGCTTACCGTAAAGCTCAAGATCTTCTGTTGAGCTTACTGCTGATATC 60
DB 16161 ATGACGAGAAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 16220
QY 61 GTTGTGCTTACGTTTCTTAAACAGGTTGTTCTGTTAAGTCTTCTGAGCTTACTATCT 120
DB 16221 GTTGTGCTTACGTTTCTTAAACAGGTTGTTCTGTTAAGTCTTCTGAGCTTACTATCT 120
QY 121 GATGTTCACTGATCTTCTGAAACATCTGCTCTGCTTCTGTTGCTGTTAAGTCTGAG 180
DB 16281 GATGTTCACTGATCTTCTGAAACATCTGCTCTGCTTCTGTTGCTGTTAAGTCTGAG 180
QY 181 AAGCAGAGGCTGCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 240
DB 16341 AAGCAGAGGCTGCTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 240
QY 241 GAGTGTGTTGTTCTTCAAGTCTCTCAAGGCTCACTTACTACTACTACTATGACT 300
DB 16401 GAGTGTGTTGTTCTTCAAGTCTCTCAAGGCTCACTTACTACTACTACTATGACT 300
QY 301 CCAGAGAGTATAG 360
DB 16461 CCAGAGAGTATAG 360
QY 361 TAGCGTAGAGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 16521 TAGCGTAGAGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

RESULT 12
US-09-939-964-1/C
; Sequence 1, Application US/09939964
; Publication No. US20030054522A1
; GENERAL INFORMATION:
; APPLICANT: Rosenthal, Andre
; APPLICANT: Freiberg, Christoph
; APPLICANT: Perret, Xavier Philippe

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; APPLICANT: Broughton, William John
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
; TITLE OF INVENTION: Plasmid
; FILE REFERENCE: CARP0068
; CURRENT APPLICATION NUMBER: US/09/939,964
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/214,808
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
; US-09-939-964-1

Query Match      20.6%; Score 94.4; DB 3; Length 536165;
Best Local Similarity 54.7%; Pred. No. 2.7e-16;
Matches 210; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 39 TGTGAGCTTACTGCTGATATCGTTGCTGCTTACGTTTAAACGAGTGTGCTGTAC 98
DB 320081 TCTTGAGCTGACAGCCGGGTGTCTGCGCTTACTGAGCCGCAATTCGTTCTGCGGC 320022
QY 99 TGAGCTTCTGAGCTTATCTCTGATGTTCACTGCACTTTCTGGAACATCT--GCTCC 155
DB 320021 CGATCTGGCAGCTTATATGACGAGCATCTCTGCTATGACGACCTCTGAGGAGA 319962
QY 156 TGCCTTCTGCTGCTTAACTGTTGAGGAGCAAGACCTGCTGTTCTGTTGTAAGTCTGT 215
DB 319961 CAAAGCTGAGAGGCTCCGCTGGAAGAACAGCCGCGCTCCGATCAAGAAAGTAGT 319902
QY 216 TCAGAGATGATCATATCGTTGTTGAGTGTGTTCTTTCAAGTCTCTCAAGCTCA 275
DB 319901 GACCGAGACTTATCATATGCTCGAGAGACGTAATAATTCGAATCGCTGAAGCACA 319842
QY 276 CCTTACTACTCATCATCTATGACTCCAGAGAGATATGAGAGAAATGTTCTTCTGT 335
DB 319841 CCTGATGCTAAGTACGAGCCCTCAAGCCGCAATATGAGAGAAATGAGGCTCTCCGCGC 319782
QY 336 TGATTACCTATGTTGCTGCTGCTTACGCTGAGGCTGTTCTGCTGCTTAAAGAGAT 395
DB 319781 TGATTACCTATGTTGCTGCTTACGCTGCTTAAAGGCTGTTCTGCTGCTTAAAGAGAT 319722
QY 396 GGGTCTCGTCAAGCTGTAAGGC 419
DB 319721 GGGTCTCGGAAAGAAAGGAGCGGC 319698

RESULT 13
US-10-465-217-13/c
; Sequence 13, Application US/10465217
; Publication No. US20030204859A1
; GENERAL INFORMATION:
; APPLICANT: Kazemi-Bafarjani, Parisa
; APPLICANT: Benzer, Seymour
; TITLE OF INVENTION: AN ANIMAL MODEL OF POLYGLUTAMINE
; TITLE OF INVENTION: TOXICITY, METHODS OF USE, AND MODULATORS OF POLYGLUTAMINE
; TITLE OF INVENTION: TOXICITY
; FILE REFERENCE: 06618-685001
; CURRENT APPLICATION NUMBER: US/10/465,217
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US/09/639,207
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: US 60/148,934
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: US 60/148,933
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: US 60/177,047
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/205,720
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 69

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
; US-10-465-217-13

Query Match      14.8%; Score 68; DB 7; Length 486;
Best Local Similarity 48.7%; Pred. No. 8.4e-10;
Matches 185; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

QY 8 AGACTCTTACGCTTAAGCTCAGATCTTCTGTTAGCTTACTGCTGATATGCTGCTG 67
DB 447 AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 368
QY 68 CTTAAGTTTCTAACACAGTGTGCTGTTACTGAGCTTCTGAGACTTATCTGATGTTTC 127
DB 387 CTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 328
QY 128 ATATGCACTTCTGGAACATGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 187
DB 327 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 268
QY 188 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
DB 267 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 208
QY 248 GTGCTTCTTCAAGTCTCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 307
DB 207 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148
QY 308 AGTATGAGAGAGTGGAGCTTCTGTTGATTACCTAATGTTGCTGCTGCTGCTGCTGCTG 367
DB 147 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 88
QY 368 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 387
DB 87 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 68

RESULT 14
US-09-894-273-1/c
; Sequence 1, Application US/09894273
; Publication No. US20040037847A1
; GENERAL INFORMATION:
; APPLICANT: Kieff, Elliott D.
; APPLICANT: Ballester, Mary E.
; APPLICANT: Kaye, Kenneth M.
; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
; TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; CURRENT APPLICATION NUMBER: US/09/894,273
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/109,422
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
; US-09-894-273-1

Query Match      14.0%; Score 64; DB 3; Length 3489;
Best Local Similarity 46.9%; Pred. No. 3.8e-08;
Matches 199; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 5 CTGAGACTGCTTACGGAAGCTCAGGATCTTCTTGAAGCTTACTGATATGATGTTG 64
DB 2331 CTCTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2272

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OY 65 CTGCTTAAGTTTCTAACAGGTTTCTGTTAATGAGCTTCCGAGCTTATCTGANG 124
DB 2271 CTCTGCTGCTCTGTTCAATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2212
OY 125 TTCAATACGACCTTCTGGAACAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 184
DB 2211 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2152
OY 185 AGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 244
DB 2151 CTGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2092
OY 245 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
DB 2091 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2032
OY 305 AGAGATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 364
DB 2031 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1972
OY 365 CTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
DB 1971 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1912
OY 425 GTCC 428
DB 1911 CTGC 1908
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RESULT 15

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US-10-294-804-1/c
; Sequence 1, Application US/10294804
; Publication No. US2003013948A1
; GENERAL INFORMATION:
; APPLICANT: Robertson, Erle S.
; APPLICANT: Collier, Murray A.
; TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
; FILE REFERENCE: UM-03778
; CURRENT APPLICATION NUMBER: US/10/294,804
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US/09/410,399
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-10-294-804-1
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Query Match 14.0%; Score 64; DB 7; Length 3489;
Best Local Similarity 46.9%; Pred. No. 3.8e-08;
Matches 199; Conservative 0; Mismatches 225; Indels 0; Gaps 0;
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OY 5 CTGAGACTGCTTAAGGTAAGGCTCAGAGATCTTCTGTTGAGCTTACTGCTGATATCGTTG 64
DB 2231 CTCTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2272
OY 65 CTGCTTAAGTTTCTAACAGGTTTCTGTTAATGAGCTTCCGAGCTTATCTGANG 124
DB 2271 CTCTGCTGCTCTGTTCAATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2212
OY 125 TTCAATACGACCTTCTGGAACAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 184
DB 2211 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2152
OY 185 AGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 244
DB 2151 CTGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2092
OY 245 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
```

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DB 2091 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2032
OY 305 AGAGATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 364
DB 2031 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1972
OY 365 CTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
DB 1971 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1912
OY 425 GTCC 428
DB 1911 CTGC 1908
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Search completed: May 20, 2006, 01:45:40
Job time : 1052 secs
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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

- Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
- Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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Sequence 166977, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patent version 3.3
; SEQ ID NO 166977
; LENGTH: 936
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166977

Query Match 13.1%; Score 59.8; DB 7; Length 936;
Best Local Similarity 52.2%; Pred. No. 1.6e-09;
Matches 133; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

Qy 12 TCGTTACGGTACCGCTCAGATCTCTTCTGTTGAGCTTACGCTGATATCGTTGCTGTTA 71
Db 281 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 222
Qy 72 CGTTTACACAGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTG 131
Db 221 TGTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTG 162
Qy 132 TGCATTTTGAACATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 191
Db 161 TGTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTG 102
Qy 192 TGTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTG 251
Db 101 TGTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTG 42
Qy 252 TTTCTTCAAGTCTCT 266
Db 41 TGTGCTGTTGCTGTTGCT 27

RESULT 3

US-11-217-529-75676/c
; Sequence 75676, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patent version 3.3
; SEQ ID NO 75676
; LENGTH: 2742
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75676

Query Match 11.6%; Score 53; DB 7; Length 2742;
Best Local Similarity 50.6%; Pred. No. 3.3e-07;
Matches 128; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

Qy 5 CTGAGACTGCTTACGCTGTAACGCTCAGATCTTCTGTTGAGCTTACTGCTGATATCGTTG 64
Db 825 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 766
Qy 65 CTGCTTACGTTTCTACACAGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG 124
Db 765 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 706
Qy 125 TTTATATGCACTTTTGTGGAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 184
Db 705 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 646
Qy 185 AGAAGCTGCTGTTTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTG 244
Db 645 TTTGATTTGCAATGATGCTTAACTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTG 586
Qy 245 CTGCTGCTGCTT 257
Db 585 TTTGCTGCTGCTG 573

RESULT 4

US-11-217-529-174235/c
; Sequence 174235, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patent version 3.3
; SEQ ID NO 174235
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174235

Query Match 11.2%; Score 51.4; DB 7; Length 231;
Best Local Similarity 56.1%; Pred. No. 3e-07;
Matches 97; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 6 TGAGACTGCTTACGCTGTAACGCTCAGATCTTCTGTTGAGCTTACTGCTGATATCGTTG 65
Db 190 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 131
Qy 66 TGTCTACGTTTCTTACACAGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTG 125
Db 130 TGTCTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTG 71
Qy 126 TCAATGCACTTTTGTGAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 178
Db 70 TGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 18

RESULT 5

US-11-217-529-174387/c
; Sequence 174387, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED

```

? APPLICANT: NAKAO, YOSHIHIRO
? APPLICANT: NAKAMURA, NORIHIRO
? APPLICANT: KODAMA, YUKIKO
? APPLICANT: FUJIMURA, TOMOKO
? APPLICANT: ASHIKARI, TOSHIHIKO
? TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
? FILE REFERENCE: S-38-285
? CURRENT APPLICATION NUMBER: US/11/217,529
? CURRENT FILING DATE: 2005-09-02
? PRIOR APPLICATION NUMBER: US 10/932,182
? PRIOR FILING DATE: 2004-09-02
? NUMBER OF SEQ ID NOS: 197023
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 174387
? LENGTH: 279
? TYPE: DNA
? ORGANISM: Saccharomyces pastorianus
? US-11-217-529-174387

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[illegible]

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RESULT 6
US-11-217-529-174145/c
Sequence 174145, Application US/11217529
Publication NO. US2006009612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOKOKO
APPLICANT: ASHIKARI, TOSHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 174145
LENGTH: 186
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-174145

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Query Match	11.0%	Score	50.4	DB 7:	length	186;	
Best Local Similarity	55.0%	Pred. No.	5	4e-07;			
Matches	99; conservative	Mismatches	81;	Indels	0;	Gaps	0

Oy	25	GCTCAGACATCTTCTTGTTGAGTTACTGCTATATCGTTCGTCTTAGCTTTTAACAC	84
Db	186	GCTGTGTTGTTCTTTGGTAAAGCTGCACATGAAGCTGTTGCTCAAGATTGTCCTGCTGTT	127

Oy 85 GGTGTCCTCGTACTAGAGCTTCGCGAATTCTCTGATGTCATACGACATTTTCGA 144
 Db 126 GTTGCTGCTGTTGCTGCTGCTGCTGATTTGTCGTGTTGTTGTTGTTGCTGCT 67
 Oy 145 AACATCGCTCCGCGCTTCCTGTTGCTCTTAACGTATAGAAACGACGAACCGCGCTTTCGTT 204
 Db 66 GCGCTGCTGCTGCTGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 7

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RESULT 7
US-11-217-529-5700/c
; Sequence 5700, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIYO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 5-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5700
; LENGTH: 2142
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5700

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Query Match	11.0%	Score 50.4	DB 7	Length 2142
Best Local Similarity	55.0%	Pred. 1.8e-06		
Matches	Conservative	0	No. matches 81	Indels 0
				Gaps 0
Qy	25	GCTCAGATCTCTCTGTGAGCTTACGCTGATATCTGTGCTGCTTACGTTCTAACAC	84	
Db	1168	GCTTTTGTGTCTGTGTAAGCCCGCAACTGATCTGTGTGTGATGTTGCTGCTGCTGT	1109	
Qy	85	GTTGTTCTGTACTGAGCTTCTCGAATTATCTGTGATTTCACTGCACTTTCTGSA	144	
Db	1108	GTTCTGCTGTGTGCTGCTGCTGTGATGTTGTTCTGTTGTGTTGTGTGCT	1043	
Qy	145	ACATCTGCTCTGCTTCTGTTGCTGTTAACGTTAGAAAGCAAGACCTGCTGTTCTGTT	204	
Db	1048	GCTCTGCTGCTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	989	

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RESULT 8
US-11-217-529-2946/c
; Sequence 2946, Application US/11217529
; Publication No. US2006009961241
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 8-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2946
; LENGTH: 2151
; TYPE: DNA

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ORGANISM: Saccharomyces pastorianus
US-11-217-529-2946

Query Match 10.8%; Score 49.4; DB 7; Length 2151;
Best Local Similarity 54.7%; Pred. No. 3.7e-06;
Matches 98; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 50 CTGCTGATATCGTTCGCTTACGCTTCTTAACCAAGTTCCTGCTTACTGAGCTTCCTG 109
DB 1767 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1708
QY 110 GACTTATCTGATGTTCACTGACCTTTCTGGAACATCTGCTCTTCTGCTGCTG 169
DB 1707 TTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1648
QY 170 TTAACGTTGGAAGCAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 228
DB 1647 CTGCTGTTGCTGTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1589

RESULT 9
US-11-217-529-2150/c
Sequence 2150, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2150
LENGTH: 2304
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-2150

Query Match 10.4%; Score 47.6; DB 7; Length 2304;
Best Local Similarity 50.9%; Pred. No. 1.3e-05;
Matches 113; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 12 TGCTTAAGCTAAGCTGAGATCTTCTTGAAGCTTACTGATATCGTTCGCTTA 71
DB 761 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702
QY 72 CGTTTCAACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 131
DB 701 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642
QY 132 TGCACTTCTGGAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 191
DB 641 TGTGATGCTGTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 582
QY 192 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 233
DB 581 TCCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

RESULT 10
US-11-217-529-5627/c
Sequence 5627, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5627
LENGTH: 1239
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-5627

Query Match 10.2%; Score 46.6; DB 7; Length 1239;
Best Local Similarity 50.7%; Pred. No. 2e-05;
Matches 112; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 21 TAAAGCTCAGAGATCTTCTTGTGAGCTTACTGCTGATATGCTGCTTAACTTCTAA 80
DB 1238 TACTGTTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1179
QY 81 CCAAGTTGCTCCGCTTACTGAGCTTCTGCACTTATCTGATGTTCACTGCACTTTC 140
DB 1178 TGGGGTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1119
QY 141 TGAACATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 200
DB 1118 TGCAGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1059
QY 201 TGTTCGTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
DB 1058 GATTGGGCTTGGGATTGAGATTGAGATTGAGATTGAGATTGAGATTGAGATTGAG 1018

RESULT 11
US-11-217-529-173524/c
Sequence 173524, Application US/11217529
Publication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 173524
LENGTH: 159
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-173524

Query Match 10.1%; Score 46.2; DB 7; Length 159;
Best Local Similarity 57.1%; Pred. No. 9.6e-06;
Matches 84; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 61 GTTGCTGCTAAGCTTTCTTAACCAAGTTCCTGTTACTAGAGCTTCCTGAGCTTATCTCT 120
DB 159 GTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 100
QY 121 GATGTTCACTGCACTTCTGGAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180


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RESULT 15
US-11-217-529-174534/c
; Sequence 174534, Application US/11217529
; Publication No. US2006099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174534
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174534

Query Match          9.3%; Score 42.8; DB 7; Length 1368;
Best Local Similarity 52.2%; Pred. No. 0.0003;
Matches 95; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 52 GCTGATATCGTTGCTGCTTACGTTTCAACCAAGTTTCCGTACTGAGCTTCTGGA 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 586 GATGCTGTGTGCTGCTGTGCTGTGCTGTGATGATGATGTGTGGAAGTTGTGT 527

QY 112 CTTATCTGATGTTTCACTGACCTTCTGGAACATCTGCTGCTGTTGTTGCTGT 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 526 GTTGTGCAACTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 467

QY 172 AACGTTGAGAAGCAAGACCTGCTGTGTTCTGTTGTAAGTCTGTTGAGATGATATC 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 466 GTATTGCACTGTGCTGATCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 407

QY 232 GT 233
   ||
DB 406 GT 405
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Search completed: May 20, 2006, 01:28:01
Job time : 20 secs